CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 4.6%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 DFMIQGGDF 99
|||||||||
Db 1 DFMIQGGDF 9

RESULT 21
AAG68089
ID AAG68089 standard; peptide; 9 AA.
XX
AC AAG68089;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 91-99.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 4.6%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 DFMIQGGDF 99
|||||||||
Db 1 DFMIQGGDF 9

RESULT 22
ABG79076
ID ABG79076 standard; peptide; 9 AA.
XX
AC ABG79076;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #2.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,

```
CC   radiation, chemotherapy or gene therapy. The administration of (I),
CC   preferably dendritic cell is prior to, subsequent to or concurrent with,
CC   the cancer treatment. The present sequence is a tumour antigen derived
CC   epitope for inclusion in the composition of the invention
XX
SQ   Sequence 9 AA;

  Query Match             4.6%;  Score 50;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |||||||||
Db          1 DFMIQGGDF 9


RESULT 23
ABR84374
ID   ABR84374 standard; peptide; 9 AA.
XX
AC   ABR84374;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human CypB HLA-A24 epitope, SEQ ID NO:24.
XX
KW   Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW   cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW   immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW   human; human leukocyte antigen; HLA-A24 epitope.
XX
OS   Homo sapiens.
XX
PN   JP2002365286-A.
XX
PD   18-DEC-2002.
XX
PF   18-SEP-2001; 2001JP-00283413.
XX
PR   13-NOV-2000; 2000JP-00345094.
XX
PA   (ITOY/) ITO Y.
XX
DR   WPI; 2003-508315/48.
XX
PT   A detection method of antigen specific T-cells, comprises the use of
PT   plural antigenic peptides, useful in semi-quantitative determination of
PT   cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS   Example 8; Page 10; 18pp; Japanese.
XX
CC   The invention relates to a method for the detection of antigen specific T
CC   -cells in a blood sample involving the use of a plurality of antigenic
CC   peptides. The method comprises sampling of peripheral blood monocytes;
CC   stimulation of the collected peripheral blood monocytes with antigens
CC   without direct use of antigen presenting cells; and detection of T-cells
CC   specific to the antigen in the stimulated monocytes. The method is
CC   particularly used for the detection of cancer as it can be used in semi-
CC   quantitative determination of cancer specific T-cells. It can also be
CC   used for cancer vaccine therapy for patients with cervical or prostate
CC   cancer. The method can additionally be used to monitor of cellular
CC   immunity and cancer immune therapy by detection of specific T-cell
CC   frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC   leukocyte antigen) peptides of human origin used in an example from the
CC   invention
XX
SQ   Sequence 9 AA;

  Query Match             4.6%;  Score 50;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |||||||||
Db          1 DFMIQGGDF 9


RESULT 24
ADC17702
ID   ADC17702 standard; peptide; 9 AA.
XX
AC   ADC17702;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Cyclophilin B protein amino acids 91-99.
XX
KW   cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW   allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW   cyclophilin B.
XX
OS   Synthetic.
XX
PN   WO2003020306-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002WO-JP008641.
XX
PR   29-AUG-2001; 2001JP-00260046.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Yamada A;
XX
DR   WPI; 2003-300831/29.
XX
PT   Desensitizers or allergic reaction suppressors containing peptides
PT   originating from the same antigenic substances as reaction-inducing
PT   substances, useful for preventing or treating type I allergic diseases
PT   and in cancer vaccines.
XX
PS   Claim 8; SEQ ID NO 2; 49pp; Japanese.
XX
CC   The invention relates to allergic reaction suppressors, comprising a
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 91-99 of the cyclophilin B protein.
XX
SQ   Sequence 9 AA;

  Query Match             4.6%;  Score 50;  DB 7;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |||||||||
Db          1 DFMIQGGDF 9


RESULT 25
AAY69939
ID   AAY69939 standard; peptide; 10 AA.
XX
AC   AAY69939;
XX
DT   11-APR-2000  (first entry)
XX
```

DE Human cyclophilin B peptide fragment #19.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 54; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

Query Match 4.6%; Score 50; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 KVTVKVYFDL 42
||||||||||
Db 1 KVTVKVYFDL 10

RESULT 26
AAY69935
ID AAY69935 standard; peptide; 11 AA.
XX
AC AAY69935;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #15.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 53; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;

Query Match 4.6%; Score 50; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ALIAGSVFFLL 18
||||||||||
Db 1 ALIAGSVFFLL 11

RESULT 27
AAY69938
ID AAY69938 standard; peptide; 11 AA.
XX
AC AAY69938;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #18.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 54; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;

Query Match 4.6%; Score 50; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 LIAGSVFFLLL 19
||||||||||
Db 1 LIAGSVFFLLL 11

RESULT 28

```
AAY69921
ID   AAY69921 standard; peptide; 9 AA.
XX
AC   AAY69921;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #1.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 49; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             4.5%;  Score 49;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 KFHRVIKDF 92
              |||||||||
Db          1 KFHRVIKDF 9


RESULT 29
AAB46930
ID   AAB46930 standard; peptide; 9 AA.
XX
AC   AAB46930;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 15; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;

  Query Match             4.5%;  Score 49;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 KFHRVIKDF 92
              |||||||||
Db          1 KFHRVIKDF 9


RESULT 30
AAG68088
ID   AAG68088 standard; peptide; 9 AA.
XX
AC   AAG68088;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Antitumour peptide cyclophilin B 84-92.
XX
KW   Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW   tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW   cyclophilin B gene; HLA-A2402.
XX
OS   Homo sapiens.
XX
PN   JP2001245675-A.
XX
PD   11-SEP-2001.
XX
PF   25-DEC-2000; 2000JP-00393047.
XX
PR   28-DEC-1999;   99JP-00374322.
XX
PA   (ITOY/) ITO Y.
XX
DR   WPI; 2001-610076/70.
XX
PT   New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT   lymphocytes and for treating cancer.
XX
PS   Claim 8; Page 2; 14pp; Japanese.
XX
```

CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 4.5%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 KFHRVIKDF 92
|||||||||
Db 1 KFHRVIKDF 9

RESULT 31
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 9 AA;

Query Match 4.5%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 KFHRVIKDF 92
|||||||||
Db 1 KFHRVIKDF 9

RESULT 32
ABR84373
ID ABR84373 standard; peptide; 9 AA.
XX
AC ABR84373;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:23.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate

```
CC   cancer. The method can additionally be used to monitor of cellular
CC   immunity and cancer immune therapy by detection of specific T-cell
CC   frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC   leukocyte antigen) peptides of human origin used in an example from the
CC   invention
XX
SQ   Sequence 9 AA;

  Query Match             4.5%;  Score 49;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 KFHRVIKDF 92
              |||||||||
Db          1 KFHRVIKDF 9


RESULT 33
ADC17701
ID   ADC17701 standard; peptide; 9 AA.
XX
AC   ADC17701;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Cyclophilin B protein amino acids 84-92.
XX
KW   cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW   allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW   cyclophilin B.
XX
OS   Synthetic.
XX
PN   WO2003020306-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002WO-JP008641.
XX
PR   29-AUG-2001; 2001JP-00260046.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Yamada A;
XX
DR   WPI; 2003-300831/29.
XX
PT   Desensitizers or allergic reaction suppressors containing peptides
PT   originating from the same antigenic substances as reaction-inducing
PT   substances, useful for preventing or treating type I allergic diseases
PT   and in cancer vaccines.
XX
PS   Claim 8; SEQ ID NO 1; 49pp; Japanese.
XX
CC   The invention relates to allergic reaction suppressors, comprising a
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 84-92 of the cyclophilin B protein.
XX
SQ   Sequence 9 AA;

  Query Match             4.5%;  Score 49;  DB 7;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 KFHRVIKDF 92
              |||||||||
Db          1 KFHRVIKDF 9


RESULT 34
AAY69950
ID   AAY69950 standard; peptide; 8 AA.
XX
AC   AAY69950;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #30.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 57; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 8 AA;

  Query Match             4.4%;  Score 48;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGKHVV 160
              ||||||||
Db          1 WLDGKHVV 8


RESULT 35
AAR72947
ID   AAR72947 standard; peptide; 14 AA.
XX
AC   AAR72947;
XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   29-NOV-1995  (first entry)
XX
DE   E. coli PPIase-alpha tryptic fragment 4.
XX
KW   Escherichia coli; protein conformation; folding; acceleration;
KW   PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KW   isomerisation; prolyl peptide bond.
XX
OS   Escherichia coli; (ST 249 strain).
```

XX
PN EP647714-A1.
XX
PD 12-APR-1995.
XX
PF 19-JUL-1990; 94EP-00203612.
XX
PR 19-JUL-1989; 89JP-00184738.
PR 06-OCT-1989; 89JP-00260244.
PR 29-DEC-1989; 89JP-00344705.
PR 19-JUL-1990; 90EP-00307914.
XX
PA (TOFU) TONEN CORP.
XX
PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
DR WPI; 1995-140756/19.
XX
PT New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate
PT the folding of proteins, partic. for activation of inactive recombinant
PT proteins.
XX
PS Example 7; Page 30; 85pp; English.
XX
CC AAR72945-48 are tryptic fragments of E. coli PPIase-alpha (peptidyl
CC prolyl cis trans isomerase). The E. coli PPIase-beta has a single mol.
CC wt. of about 22 kDa and a single isoelectric point of about 9.7. The
CC enzyme catalyses the isomerisation of prolyl peptide bonds in proteins
CC and accelerates the folding of the protein. The inventors are claiming a
CC PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
CC -MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 14 AA;

Query Match 4.4%; Score 48; DB 2; Length 14;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         88 VIKDFMIQGGDFT 100
              ||  |||||| ||
Db          1 VIPGFMIQGGGFT 13
```

RESULT 36
AAR72903
ID AAR72903 standard; peptide; 14 AA.
XX
AC AAR72903;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
DE E. coli PPIase-alpha tryptic fragment 4.
XX
KW Escherichia coli; protein conformation; folding; acceleration;
KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KW isomerisation; prolyl peptide bond.
XX
OS Escherichia coli; (ST 249 strain).
XX
PN EP647713-A1.
XX
PD 12-APR-1995.
XX
PF 19-JUL-1990; 94EP-00203610.
XX
PR 19-JUL-1989; 89JP-00184738.
PR 06-OCT-1989; 89JP-00260244.
PR 29-DEC-1989; 89JP-00344705.
PR 19-JUL-1990; 90EP-00307914.
XX
PA (TOFU) TONEN CORP.
XX
PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
DR WPI; 1995-140755/19.
XX
PT New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
PT the folding of proteins, partic. for activation of inactive recombinant
PT proteins.
XX
PS Example 7; Page 30; 85pp; English.
XX
CC AAR72900-04 are tryptic fragments of E. coli PPIase-alpha (peptidyl
CC prolyl cis trans isomerase). The E. coli PPIase-beta has a single mol.
CC wt. of about 22 kDa and a single isoelectric point of about 9.7. The
CC enzyme catalyses the isomerisation of prolyl peptide bonds in proteins
CC and accelerates the folding of the protein. The inventors are claiming
CC the PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 14 AA;

Query Match 4.4%; Score 48; DB 2; Length 14;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         88 VIKDFMIQGGDFT 100
              ||  |||||| ||
Db          1 VIPGFMIQGGGFT 13
```

RESULT 37
AAY69963
ID AAY69963 standard; peptide; 9 AA.
XX
AC AAY69963;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #43.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

```
  Query Match             4.3%;  Score 47;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |:|||||||
Db          1 DYMIQGGDF 9
```

```
RESULT 38
AAB46947
ID   AAB46947 standard; peptide; 9 AA.
XX
AC   AAB46947;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 20; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;
```

```
  Query Match             4.3%;  Score 47;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |:|||||||
Db          1 DYMIQGGDF 9
```

```
RESULT 39
ADC17709
ID   ADC17709 standard; peptide; 9 AA.
XX
AC   ADC17709;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Modified cyclophilin B protein amino acids 91-99.
XX
KW   cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW   allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW   cyclophilin B.
XX
OS   Synthetic.
XX
PN   WO2003020306-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002WO-JP008641.
XX
PR   29-AUG-2001; 2001JP-00260046.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Yamada A;
XX
DR   WPI; 2003-300831/29.
XX
PT   Desensitizers or allergic reaction suppressors containing peptides
PT   originating from the same antigenic substances as reaction-inducing
PT   substances, useful for preventing or treating type I allergic diseases
PT   and in cancer vaccines.
XX
PS   Claim 8; SEQ ID NO 9; 49pp; Japanese.
XX
CC   The invention relates to allergic reaction suppressors, comprising a
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 91-99 of the cyclophilin B protein with the
CC   Phe at position 92 replaced by a Tyr.
XX
SQ   Sequence 9 AA;
```

```
  Query Match             4.3%;  Score 47;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 DFMIQGGDF 99
              |:|||||||
Db          1 DYMIQGGDF 9
```

```
RESULT 40
AAY69962
ID   AAY69962 standard; peptide; 9 AA.
XX
AC   AAY69962;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #42.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
```

KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 4.2%; Score 46; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 84 KFHRVIKDF 92
|:|||||||
Db 1 KYHRVIKDF 9

RESULT 41
AAY69941
ID AAY69941 standard; peptide; 9 AA.
XX
AC AAY69941;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #21.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 55; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 4.2%; Score 46; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 DLRIGDEDV 49
||||||||||
Db 1 DLRIGDEDV 9

RESULT 42
AAB46946
ID AAB46946 standard; peptide; 9 AA.
XX
AC AAB46946;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 19; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 4.2%; Score 46; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          84 KFHRVIKDF 92
               |:|||||||
Db           1 KYHRVIKDF 9
```

RESULT 43
AAY69937
ID AAY69937 standard; peptide; 10 AA.
XX
AC AAY69937;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #17.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 53; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

Query Match 4.2%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           9 LIAGSVFFLL 18
               ||||||||||
Db           1 LIAGSVFFLL 10
```

RESULT 44
AAY69934
ID AAY69934 standard; peptide; 10 AA.
XX
AC AAY69934;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #14.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 53; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 10 AA;

Query Match 4.2%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           8 ALIAGSVFFL 17
               ||||||||||
Db           1 ALIAGSVFFL 10
```

RESULT 45
AAY69933
ID AAY69933 standard; peptide; 11 AA.
XX
AC AAY69933;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #13.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 52; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The

CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;

Query Match 4.2%; Score 46; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 LLAAALIAGSV 14
              ||||||||||
Db          1 LLAAALIAGSV 11
```

Search completed: August 30, 2004, 10:49:40
Job time : 309.892 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 16.3885 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-4
Perfect score: 60
Sequence: 1 GYKNSKFHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	11	3	AAY69924	Aay69924 Human cyc
2	39	65.0	9	3	AAY69923	Aay69923 Human cyc
3	32	53.3	9	3	AAY69921	Aay69921 Human cyc
4	32	53.3	9	4	AAB46930	Aab46930 Human cyc
5	32	53.3	9	4	AAG68088	Aag68088 Antitumou
6	32	53.3	9	5	ABG79075	Abg79075 Human Cyp
7	32	53.3	9	6	ABR84373	Abr84373 Human Cyp
8	32	53.3	9	7	ADC17701	Adc17701 Cyclophil
9	30	50.0	11	2	AAR72931	Aar72931 E. coli P
10	30	50.0	11	2	AAR72887	Aar72887 E. coli P
11	29	48.3	9	3	AAY69962	Aay69962 Human cyc
12	29	48.3	9	4	AAB46946	Aab46946 Human cyc
13	29	48.3	10	3	AAB27129	Aab27129 Human CAS
14	28	46.7	9	2	AAW33943	Aaw33943 Beta1-adr
15	28	46.7	14	2	AAW33942	Aaw33942 Beta1-adr
16	28	46.7	14	5	ABJ15069	Abj15069 Human 125
17	27	45.0	9	3	AAY69959	Aay69959 Human cyc
18	27	45.0	9	7	ABR84746	Abr84746 Bovine po
19	27	45.0	11	7	ADD88599	Add88599 Influenza
20	26.5	44.2	11	2	AAW19409	Aaw19409 Anti-fung
21	26.5	44.2	11	2	AAW19455	Aaw19455 Anti-fung
22	26.5	44.2	12	2	AAW19415	Aaw19415 Anti-fung
23	26.5	44.2	12	2	AAW19417	Aaw19417 Anti-fung
24	26.5	44.2	12	2	AAW19414	Aaw19414 Anti-fung
25	26.5	44.2	12	2	AAW19407	Aaw19407 Anti-fung
26	26.5	44.2	12	2	AAW19426	Aaw19426 Anti-fung
27	26.5	44.2	12	2	AAW19454	Aaw19454 Anti-fung
28	26.5	44.2	12	2	AAW19461	Aaw19461 Anti-fung
29	26.5	44.2	12	2	AAW19460	Aaw19460 Anti-fung
30	26.5	44.2	12	2	AAW19463	Aaw19463 Anti-fung
31	26.5	44.2	12	2	AAW19472	Aaw19472 Anti-fung
32	26.5	44.2	12	2	AAY25141	Aay25141 Antibacte
33	26.5	44.2	12	2	AAY25143	Aay25143 Antibacte
34	26.5	44.2	12	2	AAY25140	Aay25140 Antibacte
35	26.5	44.2	12	3	AAB11990	Aab11990 Histatin-
36	26.5	44.2	12	3	AAB11976	Aab11976 Histatin-
37	26.5	44.2	12	3	AAB11985	Aab11985 Histatin-
38	26.5	44.2	12	3	AAB11987	Aab11987 Histatin-
39	26.5	44.2	12	3	AAB11977	Aab11977 Histatin-
40	26.5	44.2	12	7	ADB81288	Adb81288 Biologica
41	26.5	44.2	14	2	AAR89887	Aar89887 Human his
42	26.5	44.2	14	2	AAW19441	Aaw19441 Anti-fung
43	26.5	44.2	14	2	AAW19452	Aaw19452 Anti-fung
44	26.5	44.2	14	2	AAW31675	Aaw31675 Human his
45	26	43.3	9	2	AAW49599	Aaw49599 Human leu

ALIGNMENTS

RESULT 1
AAY69924
ID AAY69924 standard; peptide; 11 AA.
XX
AC AAY69924;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #4.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 50; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYKNSKFHRVI 11
|||||||||||

```
Db          1 GYKNSKFHRVI 11


RESULT 2
AAY69923
ID   AAY69923 standard; peptide; 9 AA.
XX
AC   AAY69923;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #3.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 50; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             65.0%;  Score 39;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYKNSKF 7
              |||||||
Db          3 GYKNSKF 9


RESULT 3
AAY69921
ID   AAY69921 standard; peptide; 9 AA.
XX
AC   AAY69921;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #1.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 49; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             53.3%;  Score 32;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 KFHRVI 11
              ||||||
Db          1 KFHRVI 6


RESULT 4
AAB46930
ID   AAB46930 standard; peptide; 9 AA.
XX
AC   AAB46930;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 15; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
```

CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KFHRVI 11
||||||
Db 1 KFHRVI 6

RESULT 5
AAG68088
ID AAG68088 standard; peptide; 9 AA.
XX
AC AAG68088;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 84-92.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KFHRVI 11
||||||
Db 1 KFHRVI 6

RESULT 6
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX

SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 KFHRVI 11
              ||||||
Db          1 KFHRVI 6
```

RESULT 7
ABR84373
ID ABR84373 standard; peptide; 9 AA.
XX
AC ABR84373;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:23.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 KFHRVI 11
              ||||||
Db          1 KFHRVI 6
```

RESULT 8
ADC17701
ID ADC17701 standard; peptide; 9 AA.
XX
AC ADC17701;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cyclophilin B protein amino acids 84-92.
XX
KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX
PN WO2003020306-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002WO-JP008641.
XX
PR 29-AUG-2001; 2001JP-00260046.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Yamada A;
XX
DR WPI; 2003-300831/29.
XX
PT Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 1; 49pp; Japanese.
XX
CC The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet dos not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 84-92 of the cyclophilin B protein.
XX
SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 KFHRVI 11
              ||||||
Db          1 KFHRVI 6
```

RESULT 9
AAR72931
ID AAR72931 standard; peptide; 11 AA.
XX
AC AAR72931;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
DE E. coli PPIase-beta tryptic fragment 2.
XX
KW Escherichia coli; protein conformation; folding; acceleration;

KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KW isomerisation; prolyl peptide bond.
XX
OS Escherichia coli; (ST 249 strain).
XX
PN EP647714-A1.
XX
PD 12-APR-1995.
XX
PF 19-JUL-1990; 94EP-00203612.
XX
PR 19-JUL-1989; 89JP-00184738.
PR 06-OCT-1989; 89JP-00260244.
PR 29-DEC-1989; 89JP-00344705.
PR 19-JUL-1990; 90EP-00307914.
XX
PA (TOFU) TONEN CORP.
XX
PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
DR WPI; 1995-140756/19.
XX
PT New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate
PT the folding of proteins, partic. for activation of inactive recombinant
PT proteins.
XX
PS Example 6; Page 24; 85pp; English.
XX
CC AAR72930-36 are tryptic fragments of E. coli PPIase-beta (peptidyl prolyl
CC cis trans isomerase). The E. coli PPIase-beta has a single mol. wt. of
CC about 20 kDa and a single isoelectric point of about 5.0. The enzyme
CC catalyses the isomerisation of prolyl peptide bonds in proteins and
CC accelerates the folding of the protein. The inventors are claiming a
CC PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
CC -MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 50.0%; Score 30; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YKNSKFHR 9
| |: |||
Db 4 YNNTIFHR 11

RESULT 10
AAR72887
ID AAR72887 standard; peptide; 11 AA.
XX
AC AAR72887;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
DE E. coli PPIase-beta tryptic fragment 2.
XX
KW Escherichia coli; protein conformation; folding; acceleration;
KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KW isomerisation; prolyl peptide bond.
XX
OS Escherichia coli; (ST 249 strain).
XX
PN EP647713-A1.
XX
PD 12-APR-1995.
XX
PF 19-JUL-1990; 94EP-00203610.
XX
PR 19-JUL-1989; 89JP-00184738.
PR 06-OCT-1989; 89JP-00260244.
PR 29-DEC-1989; 89JP-00344705.
PR 19-JUL-1990; 90EP-00307914.
XX
PA (TOFU) TONEN CORP.
XX
PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
DR WPI; 1995-140755/19.
XX
PT New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
PT the folding of proteins, partic. for activation of inactive recombinant
PT proteins.
XX
PS Example 6; Page 24; 85pp; English.
XX
CC AAR72886-92 are tryptic fragments of E. coli PPIase-beta (peptidyl prolyl
CC cis trans isomerase). The E. coli PPIase-beta has a single mol. wt. of
CC about 20 kDa and a single isoelectric point of about 5.0. The enzyme
CC catalyses the isomerisation of prolyl peptide bonds in proteins and
CC accelerates the folding of the protein. The inventors are claiming the
CC PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 50.0%; Score 30; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YKNSKFHR 9
| |: |||
Db 4 YNNTIFHR 11

RESULT 11
AAY69962
ID AAY69962 standard; peptide; 9 AA.
XX
AC AAY69962;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #42.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that

CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 48.3%; Score 29; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 KFHRVI 11
              |:||||
Db          1 KYHRVI 6
```

RESULT 12
AAB46946
ID AAB46946 standard; peptide; 9 AA.
XX
AC AAB46946;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 19; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 48.3%; Score 29; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 KFHRVI 11
              |:||||
Db          1 KYHRVI 6
```

RESULT 13
AAB27129
ID AAB27129 standard; protein; 10 AA.
XX
AC AAB27129;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human CASB619 protein epitope SEQ ID NO: 55.
XX
KW Human; CASB619; cancer; autoimmune disease; immunogen; vaccine; epitope.
XX
OS Homo sapiens.
XX
PN WO200058460-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-EP002478.
XX
PR 26-MAR-1999; 99GB-00007113.
PR 25-SEP-1999; 99GB-00022858.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck CEM, Cassart J, Coche T, Vinals Y De BassolsC;
XX
DR WPI; 2000-664923/64.
XX
PT Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT prophylactic and therapeutic treatment of, cancers, particularly ovarian
PT and colon carcinoma, and autoimmune diseases.
XX
PS Example 7; Page 64; 68pp; English.
XX
CC The present sequence comprises an epitope derived from the human CASB619
CC protein sequence. This protein is thought to be specifically or over-
CC expressed in tumour cells, and so can be used as a target for antigen-
CC specific immune responses which can cause destruction of the tumour cell.
CC In addition, the protein and gene can be used in cancer diagnosis, in the
CC treatment of autoimmune diseases and in vaccines against cancer and
CC autoimmune disease. The present sequence can be used as an immunogen
XX
SQ Sequence 10 AA;

Query Match 48.3%; Score 29; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GYKNSKFH 8
              | ||:| |
Db          1 GTKNNKIH 8
```

RESULT 14
AAW33943
ID AAW33943 standard; peptide; 9 AA.
XX
AC AAW33943;
XX
DT 28-MAY-1998 (first entry)
XX
DE Beta1-adrenergic receptor antagonist.
XX
KW Antagonist; integral membrane protein; inhibitor; transmembrane domain;
KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
KW post-myocardial infarction; HIV infection; cell proliferation disorder;
KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
KW antibacterial; beta1-adrenergic receptor.

XX
OS Homo sapiens.
XX
PN WO9735881-A2.
XX
PD 02-OCT-1997.
XX
PF 26-MAR-1997; 97WO-CA000203.
XX
PR 27-MAR-1996; 96US-0014306P.
PR 25-JUN-1996; 96US-00670119.
PR 20-AUG-1996; 96US-0024240P.
XX
PA (NGGY/) NG G Y K.
PA (SEEM/) SEEMAN P.
PA (GEOR/) GEORGE S R.
PA (ODOW/) O'DOWD B F.
XX
PI Ng GYK, Seeman P, George SR, Odowd BF;
XX
DR WPI; 1997-489566/45.
XX
PT Inhibitor of integral membrane protein - used to treat e.g.
PT schizophrenia, hypertension, viral infection, cancer etc.
XX
PS Claim 17; Page 94; 127pp; English.
XX
CC This sequence is a beta1-adrenergic receptor antagonist, and is an
CC antagonist of the invention. The antagonists (A) are for inhibiting the
CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)
CC having at least one transmembrane domain (TMD), comprises a peptide
CC including at least 4 consecutive amino acids (aa) from the sequence of
CC the TMD. (A) are used to treat or prevent disorders in mammals that
CC involve disturbances of IMP, and the same effect is achieved by inserting
CC a nucleic acid encoding (A) into the cells of the mammal. Specified
CC conditions that can be treated are schizophrenia, psychotic disorders,
CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
CC renal disease, Parkinson's disease, congestive heart failure, migraine,
CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
CC diseases, graft rejection etc. (A) can be used as diuretics and
CC antibacterials. (A) may also be used to determine function of orphan
CC receptors and, when attached to a marker, for tissue imaging to
CC localise/quantify specific receptors. The transgenic animals are used to
CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
CC specific and selective, against the IMP from which they are derived, so
CC should have few side effects
XX
SQ Sequence 9 AA;

Query Match 46.7%; Score 28; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GYKNSKFH 8
              || || |:
Db          1 GYANSAFN 8
```

RESULT 15
AAW33942
ID AAW33942 standard; peptide; 14 AA.
XX
AC AAW33942;
XX
DT 28-MAY-1998 (first entry)
XX
DE Beta1-adrenergic receptor antagonist.
XX
KW Antagonist; integral membrane protein; inhibitor; transmembrane domain;
KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
KW post-myocardial infarction; HIV infection; cell proliferation disorder;
KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
KW antibacterial; beta1-adrenergic receptor.
XX
OS Homo sapiens.
XX
PN WO9735881-A2.
XX
PD 02-OCT-1997.
XX
PF 26-MAR-1997; 97WO-CA000203.
XX
PR 27-MAR-1996; 96US-0014306P.
PR 25-JUN-1996; 96US-00670119.
PR 20-AUG-1996; 96US-0024240P.
XX
PA (NGGY/) NG G Y K.
PA (SEEM/) SEEMAN P.
PA (GEOR/) GEORGE S R.
PA (ODOW/) O'DOWD B F.
XX
PI Ng GYK, Seeman P, George SR, Odowd BF;
XX
DR WPI; 1997-489566/45.
XX
PT Inhibitor of integral membrane protein - used to treat e.g.
PT schizophrenia, hypertension, viral infection, cancer etc.
XX
PS Claim 17; Page 94; 127pp; English.
XX
CC This sequence is a beta1-adrenergic receptor antagonist, and is an
CC antagonist of the invention. The antagonists (A) are for inhibiting the
CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)
CC having at least one transmembrane domain (TMD), comprises a peptide
CC including at least 4 consecutive amino acids (aa) from the sequence of
CC the TMD. (A) are used to treat or prevent disorders in mammals that
CC involve disturbances of IMP, and the same effect is achieved by inserting
CC a nucleic acid encoding (A) into the cells of the mammal. Specified
CC conditions that can be treated are schizophrenia, psychotic disorders,
CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
CC renal disease, Parkinson's disease, congestive heart failure, migraine,
CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
CC diseases, graft rejection etc. (A) can be used as diuretics and
CC antibacterials. (A) may also be used to determine function of orphan
CC receptors and, when attached to a marker, for tissue imaging to
CC localise/quantify specific receptors. The transgenic animals are used to
CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
CC specific and selective, against the IMP from which they are derived, so
CC should have few side effects
XX
SQ Sequence 14 AA;

Query Match 46.7%; Score 28; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GYKNSKFH 8
              || || |:
Db          6 GYANSAFN 13
```

RESULT 16
ABJ15069
ID ABJ15069 standard; peptide; 14 AA.
XX
AC ABJ15069;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3695.

XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Eid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 *gene or a molecule* that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 216; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 14 AA;

Query Match 46.7%; Score 28; DB 5; Length 14;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YKNSKFH 8
|:|:||
Db 4 YENTHFH 10

RESULT 17
AAY69959
ID AAY69959 standard; peptide; 9 AA.
XX
AC AAY69959;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #39.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 61; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 45.0%; Score 27; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FHRVI 11
|||||
Db 2 FHRVI 6

RESULT 18
ABR84746
ID ABR84746 standard; protein; 9 AA.
XX
AC ABR84746;
XX
DT 18-DEC-2003 (first entry)
XX
DE Bovine polypyrimidine tract binding protein conserved nonapeptide.
XX
KW Cow; polypyrimidine tract protein; isoform; RNA stability regulation;
KW immunosuppressive; allograft rejection; CD154; PTB.
XX
OS Bos taurus.
XX
PN WO2003061581-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001623.
XX
PR 17-JAN-2002; 2002US-0349869P.
PR 02-JAN-2003; 2003US-0437779P.
XX
PA (DART-) DARTMOUTH COLLEGE.
XX
PI Rigby WFC;
XX
DR WPI; 2003-778776/73.
XX
PT A new polypyrimidine tract protein isoform useful for finding agents
PT which modulate its activity and to prevent or treat allograft rejection
PT or CD40 activation.
XX
PS Disclosure; Page 64; 0pp; English.
XX
CC The present invention provides the protein sequence of a polypyrimidine
CC tract protein isoform. Also provided are methods for modulating the
CC stability of a CD154 RNA. The methods are useful for increasing the
CC stability of a RNA, decreasing the stability of a RNA, preventing or
CC treating allograft rejection in a subject, inhibiting CD40 activation in
CC a subject, and identifying agents that modulate the level or activity of
CC a polypyrimidine tract protein. Agents which modulate the activity of a
CC polypyrimidine tract protein are useful to prevent or treat allograft
CC rejection or inhibit CD40 activation. The present sequence is a
CC nonapeptide conserved between the bovine and human polypyrimidine tract
CC protein
XX

```
SQ   Sequence 9 AA;

  Query Match             45.0%;  Score 27;  DB 7;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+06;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YKNSKFHR 9
              | ||  ||
Db          2 YGNSPLHR 9


RESULT 19
ADD88599
ID   ADD88599 standard; peptide; 11 AA.
XX
AC   ADD88599;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Influenza virus H3N2 Replikin #4.
XX
KW   vaccine; gene therapy; malaria; influenza; Replikin; haemagglutinin.
XX
OS   Orthomyxoviridae.
XX
PN   US2003180328-A1.
XX
PD   25-SEP-2003.
XX
PF   26-MAR-2002; 2002US-00105232.
XX
PR   27-MAR-2001; 2001US-0278761P.
PR   09-JUL-2001; 2001US-0303396P.
PR   26-OCT-2001; 2001US-00984057.
XX
PA   (BOGO/) BOGOCH S.
PA   (BOGO/) BOGOCH E S.
XX
PI   Bogoch S,  Bogoch ES;
XX
DR   WPI; 2003-852213/79.
XX
PT   New Replikin peptides of Plasmodium falciparum or influenza virus, useful
PT   for diagnosing, preventing or treating influenza virus infection or
PT   malaria.
XX
PS   Disclosure; SEQ ID NO 266; 136pp; English.
XX
CC   The invention relates to an isolated Plasmodium falciparum peptide or an
CC   influenza virus peptide. The composition and methods are useful in
CC   diagnosing, preventing or treating influenza virus infection or malaria.
CC   Also disclosed is an influenza virus vaccine comprising at least one
CC   isolated Replikin present in the haemagglutinin protein of an emerging
CC   strain of influenza virus and a pharmaceutical carrier and/or adjuvant
CC   and a malaria vaccine comprising at least one isolated P. falciparum
CC   Replikin and a pharmaceutical carrier. The present sequence represents
CC   the amino acid sequence of a Replikin sequence.
XX
SQ   Sequence 11 AA;

  Query Match             45.0%;  Score 27;  DB 7;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 NSKFHRV 10
              | |||  :
Db          3 NEKFHXI 9


RESULT 20
AAW19409
ID   AAW19409 standard; peptide; 11 AA.
XX
AC   AAW19409;
XX
DT   04-SEP-1997  (first entry)
XX
DE   Anti-fungal and anti-bacterial histatin-based peptide 117.
XX
KW   Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW   vaginal infection; urethral infection; mucosal infection; ear infection;
KW   respiratory infection; skin infection; ophthalmic infection;
KW   bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW   Clostridium histolyticum.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .11
FT                   /note= "At least one amino acid must have a D-
FT                   configuration"
XX
PN   WO9640768-A2.
XX
PD   19-DEC-1996.
XX
PF   07-JUN-1996;   96WO-US009374.
XX
PR   07-JUN-1995;   95US-00481888.
XX
PA   (PERI-) PERIODONTIX INC.
PA   (UYBO-) UNIV BOSTON.
XX
PI   Oppenheim FG,  Xu T,  Roberts FD,  Spacciapoli P,  Friden PM;
XX
DR   WPI; 1997-052232/05.
XX
PT   Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT   treating Candidal infections, periodontitis and caries.
XX
PS   Claim 2; Fig 1; 72pp; English.
XX
CC   The present sequence represents a specifically claimed peptide sequence,
CC   peptide 117, where at least one amino acid is in the D-configuration. The
CC   peptide preferably is modified by an acetyl or carbamyl addition at the N
CC   -terminus and/or amidation at the C-terminus. The peptide, based on the
CC   naturally occurring histidine-rich human histatins, have anti- fungal and
CC   anti-bacterial activity and are useful in compositions for the treatment
CC   of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
CC   ophthalmic fungal or bacterial infections. It is particularly effective
CC   against local and systemic Candida albicans infection, against oral
CC   bacterial diseases such as caries and periodontitis (by inhibiting e.g.
CC   Streptococcus mutans and Porphyromonas gingivalis) and against
CC   Clostridium histolyticum. The peptide has superior anti-fungal
CC   (especially anti-Candidal) and anti-bacterial activity, particularly on a
CC   weight basin, compared to the longer, naturally occurring histatins.
CC   Peptides containing D-residues are also more resistant to degradation
CC   than L-amino acid versions
XX
SQ   Sequence 11 AA;

  Query Match             44.2%;  Score 26.5;  DB 2;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GYKNSKFH 8
              |||  |||
Db          5 GYKR-KFH 11


RESULT 21
AAW19455
ID   AAW19455 standard; peptide; 11 AA.
XX
AC   AAW19455;
XX
```

DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 117.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .11
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 117, where
CC at least one amino acid in the peptide is in the D-configuration. The
CC peptide is preferably modified by an acetyl or carbamyl addition at the N
CC -terminus and/or amidation at the C-terminus. The novel D-amino acid-
CC containing peptide, based on the naturally occurring histidine-rich human
CC histatins, have anti-fungal and anti-bacterial activity and are useful in
CC compositions for the treatment of oral, vaginal, urethral, mucosal,
CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
CC is particularly effective against local and systemic Candida albicans
CC infection, against oral bacterial diseases such as caries and
CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
CC gingivalis) and against Clostridium histolyticum. The D-amino acid-
CC containing peptide has superior anti-fungal (especially anti-candidal)
CC and anti-bacterial activity, particularly on a weight basis, compared to
CC the natural L- amino acid forms of histatins and histatin-based peptides.
CC The presence of D-residues also makes the peptides more resistant to
CC degradation than corresponding L-amino acid versions
XX
SQ Sequence 11 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 5 GYKR-KFH 11

RESULT 22
AAW19415
ID AAW19415 standard; peptide; 12 AA.
XX
AC AAW19415;

XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial histatin-based peptide 113-F5.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Claim 2; Fig 1; 72pp; English.
XX
CC The present sequence represents a specifically claimed peptide sequence,
CC peptide 113-F5, where at least one amino acid is in the D-configuration.
CC The peptide preferably is modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The peptide, based on
CC the naturally occurring histidine-rich human histatins, have anti- fungal
CC and anti-bacterial activity and are useful in compositions for the
CC treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
CC ophthalmic fungal or bacterial infections. It is particularly effective
CC against local and systemic Candida albicans infection, against oral
CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
CC Streptococcus mutans and Porphyromonas gingivalis) and against
CC Clostridium histolyticum. The peptide has superior anti-fungal
CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
CC weight basin, compared to the longer, naturally occurring histatins.
CC Peptides containing D-residues are also more resistant to degradation
CC than L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 23
AAW19417
ID AAW19417 standard; peptide; 12 AA.
XX
AC AAW19417;
XX
DT 05-SEP-1997 (first entry)

XX
DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.5.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Claim 2; Fig 1; 72pp; English.
XX
CC The present sequence represents a specifically claimed peptide sequence,
CC peptide 113-F4.5, where at least one amino acid is in the D-
CC configuration. The peptide preferably is modified by an acetyl or
CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
CC The peptide, based on the naturally occurring histidine-rich human
CC histatins, have anti-fungal and anti-bacterial activity and are useful in
CC compositions for the treatment of oral, vaginal, urethral, mucosal,
CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
CC is particularly effective against local and systemic Candida albicans
CC infection, against oral bacterial diseases such as caries and
CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
CC gingivalis) and against Clostridium histolyticum. The peptide has
CC superior anti-fungal (especially anti-Candidal) and anti-bacterial
CC activity, particularly on a weight basin, compared to the longer,
CC naturally occurring histatins. Peptides containing D-residues are also
CC more resistant to degradation than L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 GYKNSKFH 8
              ||| |||
Db          6 GYKR-KFH 12
```

RESULT 24
AAW19414
ID AAW19414 standard; peptide; 12 AA.
XX
AC AAW19414;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Claim 2; Fig 1; 72pp; English.
XX
CC The present sequence represents a specifically claimed peptide sequence,
CC peptide 113-F4, where at least one amino acid is in the D-configuration.
CC The peptide preferably is modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The peptide, based on
CC the naturally occurring histidine-rich human histatins, have anti- fungal
CC and anti-bacterial activity and are useful in compositions for the
CC treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
CC ophthalmic fungal or bacterial infections. It is particularly effective
CC against local and systemic Candida albicans infection, against oral
CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
CC Streptococcus mutans and Porphyromonas gingivalis) and against
CC Clostridium histolyticum. The peptide has superior anti-fungal
CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
CC weight basin, compared to the longer, naturally occurring histatins.
CC Peptides containing D-residues are also more resistant to degradation
CC than L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 GYKNSKFH 8
              ||| |||
Db          6 GYKR-KFH 12
```

RESULT 25
AAW19407
ID AAW19407 standard; peptide; 12 AA.
XX
AC AAW19407;
XX
DT 04-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial histatin-based peptide 113.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;

KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Claim 2; Fig 1; 72pp; English.
XX
CC The present sequence represents a specifically claimed peptide sequence,
CC peptide 113, where at least one amino acid is in the D-configuration. The
CC peptide preferably is modified by an acetyl or carbamyl addition at the N
CC -terminus and/or amidation at the C-terminus. The peptide, based on the
CC naturally occurring histidine-rich human histatins, have anti- fungal and
CC anti-bacterial activity and are useful in compositions for the treatment
CC of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
CC ophthalmic fungal or bacterial infections. It is particularly effective
CC against local and systemic Candida albicans infection, against oral
CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
CC Streptococcus mutans and Porphyromonas gingivalis) and against
CC Clostridium histolyticum. The peptide has superior anti-fungal
CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
CC weight basin, compared to the longer, naturally occurring histatins.
CC Peptides containing D-residues are also more resistant to degradation
CC than L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 26
AAW19426
ID AAW19426 standard; peptide; 12 AA.
XX
AC AAW19426;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial histatin-based peptide 113-Q3.9.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Claim 2; Fig 1; 72pp; English.
XX
CC The present sequence represents a specifically claimed peptide sequence,
CC peptide 113-Q3.9, where at least one amino acid is in the D-
CC configuration. The peptide preferably is modified by an acetyl or
CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
CC The peptide, based on the naturally occurring histidine-rich human
CC histatins, have anti-fungal and anti-bacterial activity and are useful in
CC compositions for the treatment of oral, vaginal, urethral, mucosal,
CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
CC is particularly effective against local and systemic Candida albicans
CC infection, against oral bacterial diseases such as caries and
CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
CC gingivalis) and against Clostridium histolyticum. The peptide has
CC superior anti-fungal (especially anti-Candidal) and anti-bacterial
CC activity, particularly on a weight basin, compared to the longer,
CC naturally occurring histatins. Peptides containing D-residues are also
CC more resistant to degradation than L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYK-QKFH 12

RESULT 27
AAW19454
ID AAW19454 standard; peptide; 12 AA.
XX
AC AAW19454;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 113.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.

XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113, where
CC at least one amino acid in the peptide is in the D-configuration. The
CC peptide is preferably modified by an acetyl or carbamyl addition at the N
CC -terminus and/or amidation at the C-terminus. The novel D-amino acid-
CC containing peptide, based on the naturally occurring histidine-rich human
CC histatins, have anti-fungal and anti-bacterial activity and are useful in
CC compositions for the treatment of oral, vaginal, urethral, mucosal,
CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
CC is particularly effective against local and systemic Candida albicans
CC infection, against oral bacterial diseases such as caries and
CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
CC gingivalis) and against Clostridium histolyticum. The D-amino acid-
CC containing peptide has superior anti-fungal (especially anti-candidal)
CC and anti-bacterial activity, particularly on a weight basis, compared to
CC the natural L- amino acid forms of histatins and histatin-based peptides.
CC The presence of D-residues also makes the peptides more resistant to
CC degradation than corresponding L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 28
AAW19461
ID AAW19461 standard; peptide; 12 AA.
XX
AC AAW19461;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 113-F5.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113-F5,
CC where at least one amino acid in the peptide is in the D-configuration.
CC The peptide is preferably modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
CC -containing peptide, based on the naturally occurring histidine-rich
CC human histatins, have anti-fungal and anti-bacterial activity and are
CC useful in compositions for the treatment of oral, vaginal, urethral,
CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
CC infections. It is particularly effective against local and systemic
CC Candida albicans infection, against oral bacterial diseases such as
CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
CC amino acid-containing peptide has superior anti-fungal (especially anti-
CC candidal) and anti-bacterial activity, particularly on a weight basis,
CC compared to the natural L- amino acid forms of histatins and histatin-
CC based peptides. The presence of D-residues also makes the peptides more
CC resistant to degradation than corresponding L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 29
AAW19460
ID AAW19460 standard; peptide; 12 AA.
XX
AC AAW19460;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 113-F4.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;

KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113-F4,
CC where at least one amino acid in the peptide is in the D-configuration.
CC The peptide is preferably modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
CC -containing peptide, based on the naturally occurring histidine-rich
CC human histatins, have anti-fungal and anti-bacterial activity and are
CC useful in compositions for the treatment of oral, vaginal, urethral,
CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
CC infections. It is particularly effective against local and systemic
CC Candida albicans infection, against oral bacterial diseases such as
CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
CC amino acid-containing peptide has superior anti-fungal (especially anti-
CC candidal) and anti-bacterial activity, particularly on a weight basis,
CC compared to the natural L- amino acid forms of histatins and histatin-
CC based peptides. The presence of D-residues also makes the peptides more
CC resistant to degradation than corresponding L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 30
AAW19463
ID AAW19463 standard; peptide; 12 AA.
XX
AC AAW19463;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 113-F4.5.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113-F4.5,
CC where at least one amino acid in the peptide is in the D-configuration.
CC The peptide is preferably modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
CC -containing peptide, based on the naturally occurring histidine-rich
CC human histatins, have anti-fungal and anti-bacterial activity and are
CC useful in compositions for the treatment of oral, vaginal, urethral,
CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
CC infections. It is particularly effective against local and systemic
CC Candida albicans infection, against oral bacterial diseases such as
CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
CC amino acid-containing peptide has superior anti-fungal (especially anti-
CC candidal) and anti-bacterial activity, particularly on a weight basis,
CC compared to the natural L- amino acid forms of histatins and histatin-
CC based peptides. The presence of D-residues also makes the peptides more
CC resistant to degradation than corresponding L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 31
AAW19472
ID AAW19472 standard; peptide; 12 AA.
XX
AC AAW19472;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 113-Q3.9.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;

KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .12
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113-Q3.9,
CC where at least one amino acid in the peptide is in the D-configuration.
CC The peptide is preferably modified by an acetyl or carbamyl addition at
CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
CC -containing peptide, based on the naturally occurring histidine-rich
CC human histatins, have anti-fungal and anti-bacterial activity and are
CC useful in compositions for the treatment of oral, vaginal, urethral,
CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
CC infections. It is particularly effective against local and systemic
CC Candida albicans infection, against oral bacterial diseases such as
CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
CC amino acid-containing peptide has superior anti-fungal (especially anti-
CC candidal) and anti-bacterial activity, particularly on a weight basis,
CC compared to the natural L- amino acid forms of histatins and histatin-
CC based peptides. The presence of D-residues also makes the peptides more
CC resistant to degradation than corresponding L-amino acid versions
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYK-QKFH 12

RESULT 32
AAY25141
ID AAY25141 standard; peptide; 12 AA.
XX
AC AAY25141;
XX
DT 27-AUG-1999 (first entry)
XX
DE Antibacterial and antifungal peptide 2.
XX
KW Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;
KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
XX
OS Unidentified.
XX
PN WO9931123-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US026513.
XX
PR 18-DEC-1997; 97US-00993235.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
XX
DR WPI; 1999-395161/33.
XX
PT Antibacterial and antifungal peptides.
XX
PS Disclosure; Page 7; 31pp; English.
XX
CC This invention describes novel substantially pure antibacterial and
CC antifungal peptides (A) containing between 13 and 20 amino acids, where
CC the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10-
CC R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or
CC absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or
CC absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another
CC basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another
CC hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent;
CC R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where
CC Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the
CC amino acid sequence. (A) can be used to treat fungal or bacterial
CC infection in a mammal. The peptides are particularly used to treat
CC candidal infection, as well as bacterial and viral infections, especially
CC vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic
CC infections. The infections that can be treated include those caused by
CC Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces
CC viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes
CC ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter
CC showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga
CC ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella
CC corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium
CC peridonticum, Peptostreptococcus nicros, Porphyromonas endodontalis,
CC Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens,
CC Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by
CC various Staphylococcal and Streptococcal species. AAY25140-Y25149 are
CC peptides used in the description of the invention
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 33
AAY25143
ID AAY25143 standard; peptide; 12 AA.
XX
AC AAY25143;
XX
DT 27-AUG-1999 (first entry)
XX
DE Antibacterial and antifungal peptide 4.
XX
KW Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;

KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
XX
OS Unidentified.
XX
PN WO9931123-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US026513.
XX
PR 18-DEC-1997; 97US-00993235.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
XX
DR WPI; 1999-395161/33.
XX
PT Antibacterial and antifungal peptides.
XX
PS Disclosure; Page 7; 31pp; English.
XX
CC This invention describes novel substantially pure antibacterial and
CC antifungal peptides (A) containing between 13 and 20 amino acids, where
CC the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10-
CC R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or
CC absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or
CC absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another
CC basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another
CC hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent;
CC R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where
CC Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the
CC amino acid sequence. (A) can be used to treat fungal or bacterial
CC infection in a mammal. The peptides are particularly used to treat
CC candidal infection, as well as bacterial and viral infections, especially
CC vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic
CC infections. The infections that can be treated include those caused by
CC Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces
CC viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes
CC ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter
CC showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga
CC ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella
CC corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium
CC peridonticum, Peptostreptococcus nicros, Porphyromonas endodontalis,
CC Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens,
CC Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by
CC various Staphylococcal and Streptococcal species. AAY25140-Y25149 are
CC peptides used in the description of the invention
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 GYKNSKFH 8
              |||  |||
Db          6 GYKR-KFH 12
```

RESULT 34
AAY25140
ID AAY25140 standard; peptide; 12 AA.
XX
AC AAY25140;
XX
DT 27-AUG-1999 (first entry)
XX
DE Antibacterial and antifungal peptide 1.
XX
KW Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;
KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
XX
OS Unidentified.
XX
PN WO9931123-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US026513.
XX
PR 18-DEC-1997; 97US-00993235.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
XX
DR WPI; 1999-395161/33.
XX
PT Antibacterial and antifungal peptides.
XX
PS Disclosure; Page 7; 31pp; English.
XX
CC This invention describes novel substantially pure antibacterial and
CC antifungal peptides (A) containing between 13 and 20 amino acids, where
CC the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10-
CC R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or
CC absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or
CC absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another
CC basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another
CC hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent;
CC R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where
CC Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the
CC amino acid sequence. (A) can be used to treat fungal or bacterial
CC infection in a mammal. The peptides are particularly used to treat
CC candidal infection, as well as bacterial and viral infections, especially
CC vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic
CC infections. The infections that can be treated include those caused by
CC Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces
CC viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes
CC ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter
CC showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga
CC ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella
CC corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium
CC peridonticum, Peptostreptococcus nicros, Porphyromonas endodontalis,
CC Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens,
CC Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by
CC various Staphylococcal and Streptococcal species. AAY25140-Y25149 are
CC peptides used in the description of the invention
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 GYKNSKFH 8
              |||  |||
Db          6 GYKR-KFH 12
```

RESULT 35
AAB11990
ID AAB11990 standard; peptide; 12 AA.
XX
AC AAB11990;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113-R3.9K.
XX
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX

OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "C-terminal amide"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacciapoli P, Rothstein DM, Friden PM;
XX
DR WPI; 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Example 6; Page 13; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11985-B11993 represent histatin-
CC related peptides used in the exemplifications of the invention. With the
CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
CC activity against Pseudomonas aeruginosa
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYK-KKFH 12

RESULT 36
AAB11976
ID AAB11976 standard; peptide; 12 AA.
XX
AC AAB11976;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113.
XX
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacciapoli P, Rothstein DM, Friden PM;
XX
DR WPI; 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Claim 4; Page 16; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11976-B11984 represent specifically
CC claimed histatin-related peptides for use in the method of the invention.
CC The present sequence corresponds to residues 4-15 of naturally-occurring
CC human histatin 3 and histatin 5 (AAB11974, AAB11975)
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 37
AAB11985
ID AAB11985 standard; peptide; 12 AA.
XX
AC AAB11985;
XX

DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113-NA.
XX
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 12
FT /note= "C-terminal amide"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacciapoli P, Rothstein DM, Friden PM;
XX
DR WPI; 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Example 4; Page 12; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11985-B11993 represent histatin-
CC related peptides used in the exemplifications of the invention. With the
CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
CC activity against Pseudomonas aeruginosa
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 38
AAB11987
ID AAB11987 standard; peptide; 12 AA.
XX
AC AAB11987;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113-Q3.9.
XX
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "C-terminal amide"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacciapoli P, Rothstein DM, Friden PM;
XX
DR WPI; 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Example 5; Page 12; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11985-B11993 represent histatin-
CC related peptides used in the exemplifications of the invention. With the
CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
CC activity against Pseudomonas aeruginosa
XX
SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 3; Length 12;

```
  Best Local Similarity   75.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GYKNSKFH 8
              |||  |||
Db          6 GYK-QKFH 12
```

RESULT 39
AAB11977
ID AAB11977 standard; peptide; 12 AA.
XX
AC AAB11977;
XX
DT 24-NOV-2000 (first entry)
XX
DE Histatin-related peptide, P-113 (D-form).
XX
KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key   Location/Qualifiers
FT Misc-difference 1. .12
FT   /note= "All D-form residues"
XX
PN WO200040204-A2.
XX
PD 13-JUL-2000.
XX
PF 07-JAN-2000; 2000WO-US000480.
XX
PR 08-JAN-1999; 99US-00226666.
XX
PA (PERI-) PERIODONTIX INC.
XX
PI Spacciapoli P, Rothstein DM, Friden PM;
XX
DR WPI; 2000-465852/40.
XX
PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX
PS Claim 5; Page 16; 27pp; English.
XX
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11976-B11984 represent specifically
CC claimed histatin-related peptides for use in the method of the invention
XX
SQ Sequence 12 AA;

```
  Query Match             44.2%;  Score 26.5;  DB 3;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GYKNSKFH 8
              |||  |||
Db          6 GYKR-KFH 12
```

RESULT 40
ADB81288
ID ADB81288 standard; peptide; 12 AA.
XX
AC ADB81288;
XX
DT 04-DEC-2003 (first entry)
XX
DE Biologically active histatin peptide (SeqID 22).
XX
KW peptide synthesis; protegrin IB-367; hybrid process; microflora;
KW antibacterial; oral mucositis; histatin.
XX
OS Synthetic.
XX
PN WO2003062266-A2.
XX
PD 31-JUL-2003.
XX
PF 22-JAN-2003; 2003WO-US001998.
XX
PR 22-JAN-2002; 2002US-0350449P.
XX
PA (INTR-) INTRABIOTICS PHARM INC.
XX
PI Merutka G, Zhu Z, Almeda SA;
XX
DR WPI; 2003-663393/62.
XX
PT Synthesizing protegrin IB-367 peptide used for treating infectious
PT diseases, by solid phase synthesis of specific side chain protected
PT peptide, using side chain non-protected arginine reagents and
PT deprotecting side chain protected peptide.
XX
PS Disclosure; Page 8; 70pp; English.
XX
CC This invention relates to a novel method for peptide synthesis.
CC Specifically, it refers to the synthesis of the protegrin IB-367 peptide
CC by a hybrid process, which comprises carrying out both solid phase
CC synthesis as well as liquid phase synthesis methods. The present
CC invention describes synthesising specific side chain protected peptide
CC fragment intermediates using non-protected arginine reagents, and
CC deprotecting the side chain protected peptide. The protegrin IB-367
CC peptide is active in vitro and in vivo against microflora, such that it
CC is described as having antibacterial properties and can be used for
CC treating oral mucositis. Furthermore it is useful for coupling to
CC therapeutic agents, reporter molecules, diagnostic agents and antibody
CC molecules. This peptide sequence is the histatin peptide (SeqID 22),
CC synthesised by the method of the invention.
XX
SQ Sequence 12 AA;

```
  Query Match             44.2%;  Score 26.5;  DB 7;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 3.3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 GYKNSKFH 8
              |||  |||
Db          6 GYKR-KFH 12
```

RESULT 41
AAR89887
ID AAR89887 standard; peptide; 14 AA.
XX
AC AAR89887;
XX
DT 25-MAR-2003 (revised)
DT 23-JUL-1996 (first entry)
XX
DE Human histatin 3 fragment, 3P4.
XX
KW Histidine-rich salivary protein; HRP; human; macaque; histatin 1;
KW histatin 3; Candida albicans; blastoconidia; inhibition; C. albicans;
KW parotid salivary secretion.
XX
OS Homo sapiens.
XX
PN US5486503-A.
XX
PD 23-JAN-1996.
XX
PF 09-AUG-1994; 94US-00287717.
XX
PR 01-NOV-1991; 91US-00786571.
PR 28-OCT-1993; 93US-00145030.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Xu T, Oppenheim FG;
XX
DR WPI; 1996-097084/10.
XX
PT Treatment of fungal infection with histatins or derived peptide(s) -
PT mostly new cpds., partic. for treating or preventing infection by Candida
PT albicans.
XX
PS Claim 3; Fig 1; 19pp; English.
XX
CC The sequences given in AAR89883-92 are peptide fragments derived from the
CC histidine-rich salivary protein, human and macaque histatin 1 and
CC histatin 3. This sequence represents residues 9-22 of human histatin 3.
CC These peptides are used to treat or prevent infection by Candida albicans
CC in human or veterinary medicine. These peptides are more active than
CC native histatins. These peptides were tested in three assays designed to
CC measure separately their effectiveness in killing of blastoconidia, in
CC killing of germinated cells, and in inhibiting the germination of C.
CC albicans. For these assays, human histatin 3 was isolated from human
CC parotid salivary secretions, and macaque histatin 1 was chemically
CC synthesised. Compositions containing these peptides may also be used in
CC the treatment of bacterial infections, e.g. Streptococcus mutans or P.
CC gingivalis, or viral infections, e.g. Herpes simplex or HIV-1. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 1 GYKR-KFH 7

RESULT 42
AAW19441
ID AAW19441 standard; peptide; 14 AA.
XX
AC AAW19441;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial histatin-based histatin 104.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .14
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
PN WO9640768-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009374.
XX
PR 07-JUN-1995; 95US-00481888.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX
DR WPI; 1997-052232/05.
XX
PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
PT treating Candidal infections, periodontitis and caries.
XX
PS Disclosure; Fig 1; 72pp; English.
XX
CC The present sequence represents histatin 104, found in human paratoid
CC secretion, where at least one amino acid is in the D-configuration. The
CC peptide preferably is modified by an acetyl or carbamyl addition at the N
CC -terminus and/or amidation at the C-terminus. The peptide, based on the
CC naturally occurring histidine-rich human histatins, have anti-fungal and
CC anti-bacterial activity and are useful in compositions for the treatment
CC of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
CC ophthalmic fungal or bacterial infections. It is particularly effective
CC against local and systemic Candida albicans infection, against oral
CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
CC Streptococcus mutans and Porphyromonas gingivalis) and against
CC Clostridium histolyticum. The peptide has superior anti-fungal
CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
CC weight basin, compared to the longer, naturally occurring histatins.
CC Peptides containing D-residues are also more resistant to degradation
CC than L-amino acid versions
XX
SQ Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 1 GYKR-KFH 7

RESULT 43
AAW19452
ID AAW19452 standard; peptide; 14 AA.
XX
AC AAW19452;
XX
DT 05-SEP-1997 (first entry)
XX
DE Anti-fungal and anti-bacterial D-amino acid peptide 104.
XX
KW Candida albicans; peridontitis; caries; tooth decay; oral infection;

KW vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .14
FT /note= "At least one amino acid must have D-
FT configuration"
XX
PN WO9640770-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009962.
XX
PR 07-JUN-1995; 95US-00485273.
XX
PA (PERI-) PERIODONTIX INC.
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX
DR WPI; 1997-052234/05.
XX
PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
PT peptide(s) - useful esp for treating Candidal infections, periodontitis
PT and caries.
XX
PS Claim 2; Fig 1; 63pp; English.
XX
CC The present sequence represents a specifically claimed example of an anti
CC -fungal and anti-bacterial D-amino acid histatin-based peptide 104, where
CC at least one amino acid in the peptide is in the D-configuration. The
CC peptide is preferably modified by an acetyl or carbamyl addition at the N
CC -terminus and/or amidation at the C-terminus. The novel D-amino acid-
CC containing peptide, based on the naturally occurring histidine-rich human
CC histatins, have anti-fungal and anti-bacterial activity and are useful in
CC compositions for the treatment of oral, vaginal, urethral, mucosal,
CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
CC is particularly effective against local and systemic Candida albicans
CC infection, against oral bacterial diseases such as caries and
CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
CC gingivalis) and against Clostridium histolyticum. The D-amino acid-
CC containing peptide has superior anti-fungal (especially anti-candidal)
CC and anti-bacterial activity, particularly on a weight basis, compared to
CC the natural L- amino acid forms of histatins and histatin-based peptides.
CC The presence of D-residues also makes the peptides more resistant to
CC degradation than corresponding L-amino acid versions
XX
SQ Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 1 GYKR-KFH 7

RESULT 44
AAW31675
ID AAW31675 standard; peptide; 14 AA.
XX
AC AAW31675;
XX
DT 27-MAR-1998 (first entry)
XX
DE Human histatin 3 based peptide 3P4.
XX
KW Histatin 3; macaque; human; treatment; fungal infection; candidiasis;
KW histidine rich protein.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5696078-A.
XX
PD 09-DEC-1997.
XX
PF 16-MAY-1995; 95US-00441914.
XX
PR 01-NOV-1991; 91US-00786571.
PR 28-OCT-1993; 93US-00145030.
PR 09-AUG-1994; 94US-00287717.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Oppenheim FG, Xu T;
XX
DR WPI; 1998-041326/04.
XX
PT Treating fungal infections - by administering histatin peptide(s).
XX
PS Claim 1; Col 11-12; 19pp; English.
XX
CC This is a human histatin 3 based peptide 3P4. Histatin is a histidine
CC rich salivary protein. This peptide and other peptides based on human
CC histatin 3 and macaque histatins can be synthesised for treatment of
CC fungal, in particular, candidal infections. Expression vectors encoding
CC these peptides can be used in antifungal treatment methods. They can be
CC used to treat candidiasis, fungal infections of the oral cavity, vagina,
CC urethra and skin and systemic fungal infections
XX
SQ Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GYKNSKFH 8
||| |||
Db 1 GYKR-KFH 7

RESULT 45
AAW49599
ID AAW49599 standard; peptide; 9 AA.
XX
AC AAW49599;
XX
DT 05-JUN-1998 (first entry)
XX
DE Human leucocyte antigen DQ4 binding peptide #490.
XX
KW Human leucocyte antigen; HLA-DQ4; combinatorial library;
KW autoimmune disease; chronic articular rheumatism.
XX
OS Synthetic.
XX
PN JP08151396-A.
XX
PD 11-JUN-1996.
XX
PF 28-NOV-1994; 94JP-00292657.
XX
PR 28-NOV-1994; 94JP-00292657.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI; 1996-329479/33.
XX
PT HLA-binding oligopeptide and an immuno:regulator contg it - used in the

PT treatment of auto:immune disease.
XX
PS Claim 4; Page 53; 61pp; Japanese.
XX
CC This peptide is an example of a peptide which binds to a human leucocyte
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
CC combinatorial library comprising the sequence AAV05953, by screening with
CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune
CC disease, or especially for treatment of viral diseases
XX
SQ Sequence 9 AA;

Query Match 43.3%; Score 26; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GYKNSKFHR 9
              |||   : |
Db          1 GYKRDSYER 9
```

Search completed: August 30, 2004, 10:49:29
Job time : 17.3885 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 200.27 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	3.1	13	6	Q865C9	Q865c9 sus scrofa
2	32	3.0	13	10	Q9AU99	Q9au99 aethionema
3	31	2.9	9	4	Q9H326	Q9h326 homo sapien
4	31	2.9	13	13	Q9PS56	Q9ps56 carassius a
5	29	2.7	13	3	P87031	P87031 saccharomyc
6	29	2.7	13	4	Q9UPE7	Q9upe7 homo sapien
7	29	2.7	13	8	Q9T4K5	Q9t4k5 bryopsis sp
8	29	2.7	13	8	Q9THS0	Q9ths0 bryopsis sp
9	29	2.7	13	8	Q9T4K4	Q9t4k4 bryopsis sp
10	29	2.7	13	8	Q9THS2	Q9ths2 bryopsis sp
11	29	2.7	13	8	Q9T4K6	Q9t4k6 bryopsis sp
12	29	2.7	13	8	Q9T4K3	Q9t4k3 bryopsis sp
13	29	2.7	14	4	Q9UNM9	Q9unm9 homo sapien
14	28	2.6	14	2	Q9LCS1	Q9lcs1 bacillus su
15	27	2.5	11	5	Q9UAR8	Q9uar8 aedes aegyp
16	27	2.5	14	2	Q9R3U3	Q9r3u3 chlamydia t
17	27	2.5	14	5	Q26100	Q26100 pratylenchu
18	27	2.5	14	6	Q9N1V6	Q9n1v6 equus cabal
19	26.5	2.4	14	2	Q52636	Q52636 escherichia
20	26	2.4	10	11	Q9QVE9	Q9qve9 mus sp. pro
21	26	2.4	12	6	Q9N2B9	Q9n2b9 gorilla gor
22	26	2.4	12	6	Q9N2B8	Q9n2b8 pongo pygma
23	26	2.4	12	6	Q9N2C0	Q9n2c0 pan troglod
24	26	2.4	12	10	Q93YC8	Q93yc8 nicotiana t
25	26	2.4	12	10	Q8GSB9	Q8gsb9 lolium pere
26	26	2.4	12	11	Q80XV4	Q80xv4 rattus sp.
27	26	2.4	12	11	Q64313	Q64313 rattus norv
28	26	2.4	13	4	Q7Z5Z6	Q7z5z6 homo sapien
29	26	2.4	13	13	P82848	P82848 rana pipien
30	26	2.4	14	15	Q8JDM3	Q8jdm3 human immun
31	26	2.4	14	15	Q8JDM7	Q8jdm7 human immun
32	26	2.4	14	15	Q8JDM0	Q8jdm0 human immun
33	25.5	2.4	13	8	Q9THS3	Q9ths3 bryopsis sp
34	25	2.3	9	2	Q84F20	Q84f20 bacillus su
35	25	2.3	9	8	Q85G96	Q85g96 pyrrhobryum
36	25	2.3	10	10	Q8SAC2	Q8sac2 amblystegiu
37	25	2.3	11	2	Q47606	Q47606 escherichia
38	25	2.3	11	4	Q9C057	Q9c057 homo sapien
39	25	2.3	12	4	Q9BQQ1	Q9bqq1 homo sapien
40	25	2.3	12	8	Q9XNR6	Q9xnr6 pylaiella l
41	25	2.3	12	10	Q8H6E6	Q8h6e6 hordeum vul
42	25	2.3	12	12	Q80IG7	Q80ig7 choristoneu
43	25	2.3	13	13	Q7ZZN7	Q7zzn7 xenopus lae
44	25	2.3	13	15	Q98YM1	Q98ym1 human immun
45	25	2.3	14	11	Q99PB8	Q99pb8 mus musculu

ALIGNMENTS

RESULT 1
Q865C9
ID Q865C9 PRELIMINARY; PRT; 13 AA.
AC Q865C9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamine synthetase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Christenson R.K.;
RT "Characterization of porcine glutamine synthetase.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY216477; AAO64254.1; -.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 3.1%; Score 34; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          73 TGEKGFGYKN 82
               ||:: | |||
Db           4 TGDEPFQYKN 13
```

RESULT 2
Q9AU99
ID Q9AU99 PRELIMINARY; PRT; 13 AA.
AC Q9AU99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chalcone synthase (Fragment).
OS Aethionema grandiflora.

```
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Aethionema.
OX   NCBI_TaxID=72657;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.;
RT   "Phylogenetic analysis of promoter sequences from cruciferous
RT   plants.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF249000; AAK31935.1; -.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1432 MW;  5C444963C4621AA7 CRC64;

  Query Match             3.0%;  Score 32;  DB 10;  Length 13;
  Best Local Similarity  60.0%;  Pred. No. 2e+04;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         21 GPSAADEKKK 30
              |||: || :|
Db          2 GPSSLDEIRK 11


RESULT 3
Q9H326
ID   Q9H326      PRELIMINARY;      PRT;     9 AA.
AC   Q9H326;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   NAD+-dependent isocitrate dehydrogenase 3 alpha subunit
DE   (Fragment).
GN   IDH3A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT   "Structural and functional characterization of the human NAD+-
RT   dependent isocitrate dehydrogenase alpha subunit promoter.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF157515; AAG43379.1; -.
FT   NON_TER      9      9
SQ   SEQUENCE   9 AA;  960 MW;  C91CB0437DC7687D CRC64;

  Query Match             2.9%;  Score 31;  DB 4;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        126 GPGWVS 131
              || |:|
Db          3 GPAWIS 8


RESULT 4
Q9PS56
ID   Q9PS56      PRELIMINARY;      PRT;    13 AA.
AC   Q9PS56;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   NEUROLIN=CELL surface glycoprotein (Fragment).
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92250720; PubMed=1577862;
RA   Paschke K.A., Lottspeich F., Stuermer C.A.;
RT   "Neurolin, a cell surface glycoprotein on growing retinal axons in the
RT   goldfish visual system, is reexpressed during retinal axonal
RT   regeneration.";
RL   J. Cell Biol. 117:863-875(1992).
FT   NON_TER      1      1
FT   NON_TER     13     13
SQ   SEQUENCE   13 AA;  1332 MW;  33AF8FF8CC535728 CRC64;

  Query Match             2.9%;  Score 31;  DB 13;  Length 13;
  Best Local Similarity  44.4%;  Pred. No. 2.4e+04;
  Matches    4;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         53 IFGLFGKTV 61
              : ||:|:|:
Db          4 VIGLYGETI 12


RESULT 5
P87031
ID   P87031      PRELIMINARY;      PRT;    13 AA.
AC   P87031;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   ORF YGR126W (Fragment).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,
RA   Nawrocki A., Del Bino S., Goffeau A.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z72912; CAA97139.2; -.
FT   NON_TER      1      1
SQ   SEQUENCE   13 AA;  1594 MW;  2954BA87F3F8C9C8 CRC64;

  Query Match             2.7%;  Score 29;  DB 3;  Length 13;
  Best Local Similarity  46.7%;  Pred. No. 3.6e+04;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    6;  Gaps    1;

Qy         74 GEKGFGYKNSKFHRV 88
              | |||       |||:
Db          3 GIKGF------FHRI 11


RESULT 6
Q9UPE7
ID   Q9UPE7      PRELIMINARY;      PRT;    13 AA.
AC   Q9UPE7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Inosine monophosphatase 2 (Fragment).
GN   IMPA2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97463449; PubMed=9322233;
RA   Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA   Detera-Wadleigh S.D.;
RT   "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT   susceptibility region for bipolar disorder.";
RL   Mol. Psychiatry 2:393-397(1997).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20284187;
RA   Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA   Esterling L.E., Detera-Wadleigh S.D.;
RT   "Genomic structure and novel variants of myo-inositol monophosphatase
RT   2.";
RL   Mol. Psychiatry 5:165-171(2000).
DR   EMBL; AF025882; AAD22136.1; -.
DR   EMBL; AF025881; AAD22136.1; JOINED.
FT   NON_TER       1      1
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1589 MW;  F3415D841F48D401 CRC64;

  Query Match             2.7%;  Score 29;  DB 4;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        113 ERFPDENF 120
              ||||   |
Db          1 ERFPSHRF 8


RESULT 7
Q9T4K5
ID   Q9T4K5      PRELIMINARY;      PRT;    13 AA.
AC   Q9T4K5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PBSH (Fragment).
GN   PBSH.
OS   Bryopsis sp. C.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103786;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170407; AAD56846.1; -.
DR   EMBL; AF170383; AAD56798.1; -.
DR   EMBL; AF170384; AAD56800.1; -.
DR   EMBL; AF170385; AAD56802.1; -.
DR   EMBL; AF170386; AAD56804.1; -.
DR   EMBL; AF170387; AAD56806.1; -.
DR   EMBL; AF170388; AAD56808.1; -.
DR   EMBL; AF170389; AAD56810.1; -.
DR   EMBL; AF170390; AAD56812.1; -.
DR   EMBL; AF170391; AAD56814.1; -.
DR   EMBL; AF170392; AAD56816.1; -.
DR   EMBL; AF170393; AAD56818.1; -.
DR   EMBL; AF170394; AAD56820.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1366 MW;  2C31687A2E93A338 CRC64;

  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 8
Q9THS0
ID   Q9THS0      PRELIMINARY;      PRT;    13 AA.
AC   Q9THS0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PbsH (Fragment).
GN   PBSH.
OS   Bryopsis sp. B.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103785;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96-15-06;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170406; AAD56844.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1351 MW;  2C316AF02E93A338 CRC64;

  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 9
Q9T4K4
ID   Q9T4K4      PRELIMINARY;      PRT;    13 AA.
AC   Q9T4K4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PBSH (Fragment).
GN   PBSH.
OS   Bryopsis sp. B.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103785;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170405; AAD56842.1; -.
DR   EMBL; AF170395; AAD56822.1; -.
DR   EMBL; AF170396; AAD56824.1; -.
DR   EMBL; AF170397; AAD56826.1; -.
DR   EMBL; AF170398; AAD56828.1; -.
DR   EMBL; AF170399; AAD56830.1; -.
DR   EMBL; AF170400; AAD56832.1; -.
DR   EMBL; AF170401; AAD56834.1; -.
DR   EMBL; AF170402; AAD56836.1; -.
DR   EMBL; AF170403; AAD56838.1; -.
DR   EMBL; AF170404; AAD56840.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1366 MW;  2C31687A2E93A338 CRC64;
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  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 10
Q9THS2
ID   Q9THS2      PRELIMINARY;      PRT;    13 AA.
AC   Q9THS2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PbsH (Fragment).
GN   PBSH.
OS   Bryopsis sp. D.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103787;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=97-07-01;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170382; AAD56796.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1366 MW;  2C31687A2E93A338 CRC64;

  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 11
Q9T4K6
ID   Q9T4K6      PRELIMINARY;      PRT;    13 AA.
AC   Q9T4K6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PBSH (Fragment).
GN   PBSH.
OS   Bryopsis sp. A.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103784;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170415; AAD56862.1; -.
DR   EMBL; AF170408; AAD56848.1; -.
DR   EMBL; AF170409; AAD56850.1; -.
DR   EMBL; AF170410; AAD56852.1; -.
DR   EMBL; AF170411; AAD56854.1; -.
DR   EMBL; AF170412; AAD56856.1; -.
DR   EMBL; AF170414; AAD56860.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1366 MW;  2C31687A2E93A338 CRC64;

  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 12
Q9T4K3
ID   Q9T4K3      PRELIMINARY;      PRT;    13 AA.
AC   Q9T4K3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PBSH (Fragment).
GN   PBSH.
OS   Bryopsis sp. E.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103788;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=95-05-03, 96-07-03, 95-12-02, 94-19-1R, 97-13-1R, and 98-08-03;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170380; AAD56792.1; -.
DR   EMBL; AF170373; AAD56778.1; -.
DR   EMBL; AF170375; AAD56782.1; -.
DR   EMBL; AF170376; AAD56784.1; -.
DR   EMBL; AF170377; AAD56786.1; -.
DR   EMBL; AF170378; AAD56788.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1366 MW;  2C31687A2E93A338 CRC64;

  Query Match             2.7%;  Score 29;  DB 8;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 3.6e+04;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        134 NAGKDT 139
              |:||||
Db          4 NSGKDT 9


RESULT 13
Q9UNM9
ID   Q9UNM9      PRELIMINARY;      PRT;    14 AA.
AC   Q9UNM9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RING3 protein (Fragment).
GN   RING3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RA   Keddache M, Zhang F, Greenberg D.A.;
RT   "A Dinucleotide Repeat Between Exons 2 and 3 of the Human RING3
RT   Gene.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF107699; AAD24963.1; -.
DR   InterPro; IPR001487; Bromodomain.
FT   NON_TER       1      1
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1677 MW;  5CDF036680AE22D3 CRC64;

  Query Match              2.7%;  Score 29;  DB 4;  Length 14;
  Best Local Similarity   41.7%;  Pred. No. 4e+04;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         85 FHRVIKDFMIQG 96
              :|::||  |  |
Db          2 YHKIIKQPMDMG 13


RESULT 14
Q9LCS1
ID   Q9LCS1      PRELIMINARY;      PRT;    14 AA.
AC   Q9LCS1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Levan sucrase (Fragment).
GN   SACB.
OS   Bacillus subtilis.
OG   Plasmid pIZ57.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maldonado R., Casadesus J.;
RT   "Identification of IS210 in Azotobacter vinelandii: a novel,
RT   functional insertion element member of the IS5 family.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ249381; CAB76429.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW   Plasmid.
FT   NON_TER       1      1
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1623 MW;  8DC9108BA1B18745 CRC64;

  Query Match              2.6%;  Score 28;  DB 2;  Length 14;
  Best Local Similarity   54.5%;  Pred. No. 4.9e+04;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        178 KTDSRDKPLKD 188
              | |: |  |||
Db          1 KFDANDSILKD 11


RESULT 15
Q9UAR8
ID   Q9UAR8      PRELIMINARY;      PRT;    11 AA.
AC   Q9UAR8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Sialokinin I preproprotein (Fragment).
OS   Aedes aegypti (Yellowfever mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX   NCBI_TaxID=7159;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX   MEDLINE=20099025; PubMed=10620041;
RA   Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
RT   "Characterization of the Sialokinin I gene encoding the salivary
RT   vasodilator of the yellow fever mosquito, Aedes aegypti.";
RL   Insect Mol. Biol. 8:459-467(1999).
DR   EMBL; AF108100; AAD16884.1; -.
DR   GO; GO:0007268; P:synaptic transmission; IEA.
DR   GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   11 AA;  1203 MW;  8BADC77C6B59C33A CRC64;

  Query Match              2.5%;  Score 27;  DB 5;  Length 11;
  Best Local Similarity   45.5%;  Pred. No. 4.4e+04;
  Matches    5;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         48 DVGRVIFGLFG 58
              | |   :|| |
Db          1 DTGDKFYGLMG 11


RESULT 16
Q9R3U3
ID   Q9R3U3      PRELIMINARY;      PRT;    14 AA.
AC   Q9R3U3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   27 kDa histone analog (Fragment).
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=813;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92041597; PubMed=1938908;
RA   Hackstadt T.;
RT   "Purification and N-terminal amino acid sequences of Chlamydia
RT   trachomatis histone analogs.";
RL   J. Bacteriol. 173:7046-7049(1991).
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1519 MW;  423ED67AE4969D03 CRC64;

  Query Match              2.5%;  Score 27;  DB 2;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 6e+04;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        171 VRKVESTKT 179
              |:|  ||||
Db          4 VQKKRSTKT 12


RESULT 17
Q26100
ID   Q26100      PRELIMINARY;      PRT;    14 AA.
AC   Q26100;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ppmsp-5 (Fragment).
GN   PPMSP-5.
OS   Pratylenchus penetrans (Root-lesion nematode).
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC   Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
OX   NCBI_TaxID=45929;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Maryland isolate;
RA   Setterquist R.A., Smith G.K., Jones R., Fox G.E.;
RT   "Diagnostic Probes Targeting the Major Sperm Protein Gene may be
RT   Useful for the Molecular Identification of Nematodes.";
RL   J. Nematol. 0:0-0(1996).
DR   EMBL; U57830; AAB02263.1; -.
FT   NON_TER       1      1
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1775 MW;  18EB70A35334554B CRC64;
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  Query Match              2.5%;  Score 27;  DB 5;  Length 14;
  Best Local Similarity   36.4%;  Pred. No. 6e+04;
  Matches    4;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        155 DGKHVVFGKVL 165
              | ||  : |::
Db          2 DDKHTYYMKII 12


RESULT 18
Q9N1V6
ID   Q9N1V6      PRELIMINARY;      PRT;    14 AA.
AC   Q9N1V6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Beta-hemoglobin (Fragment).
GN   HBB.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20082971; PubMed=10613847;
RA   Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA   Bowling A.T., Murray J.D.;
RT   "A comparative gene map of the horse (Equus caballus).";
RL   Genome Res. 9:1239-1249(1999).
DR   EMBL; AF134224; AAF63865.1; -.
FT   NON_TER       1      1
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1456 MW;  5C14536E1EEF1977 CRC64;

  Query Match              2.5%;  Score 27;  DB 6;  Length 14;
  Best Local Similarity   40.0%;  Pred. No. 6e+04;
  Matches    4;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         44 IGDEDVGRVI 53
              :| | :||::
Db          2 VGGEALGRLV 11


RESULT 19
Q52636
ID   Q52636      PRELIMINARY;      PRT;    14 AA.
AC   Q52636;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   TraL protein (Fragment).
GN   TRAL.
OS   Escherichia coli.
OG   Plasmid R124.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86059219; PubMed=2999074;
RA   Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT   "Characterization and sequence analysis of pilin from F-like
RT   plasmids.";
RL   J. Bacteriol. 164:1238-1247(1985).
DR   EMBL; K03092; AAA92759.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW   Plasmid.
FT   NON_TER       14     14
SQ   SEQUENCE   14 AA;  1713 MW;  5CCA91188EB30E23 CRC64;

  Query Match              2.4%;  Score 26.5;  DB 2;  Length 14;
  Best Local Similarity   77.8%;  Pred. No. 6.6e+04;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        117 DENFKLKHY 125
              ||| ||| |
Db          4 DEN-KLKKY 11


RESULT 20
Q9QVE9
ID   Q9QVE9      PRELIMINARY;      PRT;    10 AA.
AC   Q9QVE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Protamine MP2 intermediate protein PMP2/11 (Fragment).
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92174934; PubMed=1541289;
RA   Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT   "Molecular characterization of six intermediate proteins in the
RT   processing of mouse protamine P2 precursor.";
RL   Eur. J. Biochem. 204:759-765(1992).
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1029 MW;  FCAD2DD8676866D1 CRC64;

  Query Match              2.4%;  Score 26;  DB 11;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+04;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        124 HYGPG 128
              | |||
Db          3 HQGPG 7


RESULT 21
Q9N2B9
ID   Q9N2B9      PRELIMINARY;      PRT;    12 AA.
AC   Q9N2B9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Indolethylamine N-methyltransferase (Fragment).
GN   INMT.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=gorilla-U1;
RA   Kitano T., Kobayakawa H., Saitou N.;
RT   "Silver Project.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB041364; BAA94453.1; -.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Methyltransferase; Transferase.
FT   NON_TER       12     12
SQ   SEQUENCE   12 AA;  1289 MW;  CF0798E2917861A9 CRC64;

  Query Match              2.4%;  Score 26;  DB 6;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 6e+04;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              | || ||
Db          3 GGFTGGD 9
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RESULT 22
Q9N2B8
ID   Q9N2B8      PRELIMINARY;      PRT;    12 AA.
AC   Q9N2B8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Indolethylamine N-methyltransferase (Fragment).
GN   INMT.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=oran-Po13;
RA   Kitano T., Kobayakawa H., Saitou N.;
RT   "Silver Project.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB041365; BAA94454.1; -.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Methyltransferase; Transferase.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1290 MW;  CF079554917861A9 CRC64;

  Query Match             2.4%;  Score 26;  DB 6;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 6e+04;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              | || ||
Db          3 GGFTGGD 9


RESULT 23
Q9N2C0
ID   Q9N2C0      PRELIMINARY;      PRT;    12 AA.
AC   Q9N2C0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Indolethylamine N-methyltransferase (Fragment).
GN   INMT.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=chimp-220;
RA   Kitano T., Kobayakawa H., Saitou N.;
RT   "Silver Project.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB041363; BAA94452.1; -.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Methyltransferase; Transferase.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1289 MW;  CF0798E2917861A9 CRC64;

  Query Match             2.4%;  Score 26;  DB 6;  Length 12;
  Best Local Similarity   71.4%;  Pred. No. 6e+04;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              | || ||
Db          3 GGFTGGD 9


RESULT 24
Q93YC8
ID   Q93YC8      PRELIMINARY;      PRT;    12 AA.
AC   Q93YC8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative coat protein (Fragment).
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   van der Winden J.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20027532; PubMed=10557305;
RA   Jakowitsch J., Mette M.F., van der Winden J., Matzke M.A.,
RA   Matzke A.J.;
RT   "Integrated pararetroviral sequences define a unique class of
RT   dispersed repetitive DNA in plants.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).
DR   EMBL; AJ414170; CAC88799.1; -.
DR   GO; GO:0019028; C:viral capsid; IEA.
DR   GO; GO:0005198; F:structural molecule activity; IEA.
KW   Coat protein.
FT   NON_TER      1      1
SQ   SEQUENCE   12 AA;  1402 MW;  89226B3A0351E321 CRC64;

  Query Match             2.4%;  Score 26;  DB 10;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 6e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        123 KHYG 126
              ||||
Db          6 KHYG 9


RESULT 25
Q8GSB9
ID   Q8GSB9      PRELIMINARY;      PRT;    12 AA.
AC   Q8GSB9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ENOD40-like protein.
OS   Lolium perenne (Perennial ryegrass).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Poeae; Lolium.
OX   NCBI_TaxID=4522;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Borvi; TISSUE=Stem;
RA   Larsen K.;
RT   "ENOD40 homolog from perennial ryegrass (Lolium perenne).";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RA   Larsen K.;
RT   "ENOD40 gene from perennial ryegrass (Lolium perenne).";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF538350; AAN15133.1; -.
DR   EMBL; AF538351; AAN15134.1; -.
SQ   SEQUENCE   12 AA;  1455 MW;  3EF4B0A918EB1733 CRC64;

  Query Match             2.4%;  Score 26;  DB 10;  Length 12;
  Best Local Similarity   40.0%;  Pred. No. 6e+04;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        149 VKTAWLDGKH 158
              :: |||:  |
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```
Db          1 MEDAWLEHLH 10


RESULT 26
Q80XV4
ID   Q80XV4      PRELIMINARY;      PRT;    12 AA.
AC   Q80XV4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orf4.
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94012815; PubMed=8408077;
RA   Rao S.M., Howells R.D.;
RT   "cis-acting elements in the 5'-untranslated region of rat testis
RT   proenkephalin mRNA regulate translation of the precursor protein.";
RL   J. Biol. Chem. 268:22164-22169(1993).
DR   EMBL; S66180; AAP13974.1; -.
SQ   SEQUENCE   12 AA;  1436 MW;  D33C6D2A83B36776 CRC64;

  Query Match             2.4%;  Score 26;  DB 11;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 6e+04;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        153 WLDGKH 158
              |  |||
Db          7 WDSGKH 12


RESULT 27
Q64313
ID   Q64313      PRELIMINARY;      PRT;    12 AA.
AC   Q64313;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   ENK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fisher 344; TISSUE=Striatum;
RX   MEDLINE=90066445; PubMed=2573832;
RA   Garrett J.E., Collard M.W., Douglass J.O.;
RT   "Translational control of germ cell-expressed mRNA imposed by
RT   alternative splicing: opioid peptide gene expression in rat testis.";
RL   Mol. Cell. Biol. 9:4381-4389(1989).
DR   EMBL; K02805; AAA60733.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   12 AA;  1436 MW;  D33C6D2A83B36776 CRC64;

  Query Match             2.4%;  Score 26;  DB 11;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 6e+04;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        153 WLDGKH 158
              |  |||
Db          7 WDSGKH 12


RESULT 28
Q7Z5Z6
ID   Q7Z5Z6      PRELIMINARY;      PRT;    13 AA.
AC   Q7Z5Z6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   NPC-A-11.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shu J., Li G., He X.;
RT   "Construction of cDNA expression library from nasopharyngeal carcinoma
RT   tissue and screening of antigenic genes.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY320404; AAP73806.1; -.
SQ   SEQUENCE   13 AA;  1429 MW;  1D0C143838017694 CRC64;

  Query Match             2.4%;  Score 26;  DB 4;  Length 13;
  Best Local Similarity   71.4%;  Pred. No. 6.6e+04;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        131 SMANAGK 137
              |:|| ||
Db          3 SLANMGK 9


RESULT 29
P82848
ID   P82848      PRELIMINARY;      PRT;    13 AA.
AC   P82848;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Temporin-1P.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN;
RX   MEDLINE=20117700; PubMed=10651828;
RA   Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA   Conlon J.M.;
RT   "Peptides with antimicrobial activity from four different families
RT   isolated from the skins of the North American frogs Rana luteiventris,
RT   Rana berlandieri and Rana pipiens.";
RL   Eur. J. Biochem. 267:894-900(2000).
CC   -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM
CC       S.AUREUS.
CC   -!- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.
CC   -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
CC       FAMILY.
DR   GO; GO:0006805; P:xenobiotic metabolism; IEA.
KW   Antibiotic; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1370 MW;  3EF3402B9DF92338 CRC64;

  Query Match             2.4%;  Score 26;  DB 13;  Length 13;
  Best Local Similarity   44.4%;  Pred. No. 6.6e+04;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 VFGKVLEGM 168
              : ||:| |:
Db          4 IVGKLLSGL 12


RESULT 30
Q8JDM3
ID   Q8JDM3      PRELIMINARY;      PRT;    14 AA.
AC   Q8JDM3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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```
DE   Truncated tat protein (Fragment).
GN   TAT.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22032414; PubMed=12036486;
RA   Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT   "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT   Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT   Infecting Virus.";
RL   AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR   EMBL; AF407149; AAM66202.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   14 AA;  1442 MW;  37C58F7BF82D7AA8 CRC64;

  Query Match             2.4%;  Score 26;  DB 15;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 7.2e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTG 106
              ||| ||
Db          6 RGDPTG 11


RESULT 31
Q8JDM7
ID   Q8JDM7      PRELIMINARY;      PRT;    14 AA.
AC   Q8JDM7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Truncated tat protein (Fragment).
GN   TAT.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22032414; PubMed=12036486;
RA   Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT   "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT   Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT   Infecting Virus.";
RL   AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR   EMBL; AF407148; AAM66198.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   14 AA;  1442 MW;  37C58F7BF82D7AA8 CRC64;

  Query Match             2.4%;  Score 26;  DB 15;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 7.2e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTG 106
              ||| ||
Db          6 RGDPTG 11


RESULT 32
Q8JDM0
ID   Q8JDM0      PRELIMINARY;      PRT;    14 AA.
AC   Q8JDM0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Truncated tat protein (Fragment).
GN   TAT.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22032414; PubMed=12036486;
RA   Long E.M., Rainwater S.M., Lavreys L., Mandaliya K., Overbaugh J.;
RT   "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT   Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT   Infecting Virus.";
RL   AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR   EMBL; AF407150; AAM66205.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   14 AA;  1442 MW;  37C58F7BF82D7AA8 CRC64;

  Query Match             2.4%;  Score 26;  DB 15;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 7.2e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTG 106
              ||| ||
Db          6 RGDPTG 11


RESULT 33
Q9THS3
ID   Q9THS3      PRELIMINARY;      PRT;    13 AA.
AC   Q9THS3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PbsH (Fragment).
GN   PBSH.
OS   Bryopsis sp. D.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC   Bryopsidaceae; Bryopsis.
OX   NCBI_TaxID=103787;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=96-21-02;
RA   Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT   "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT   Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT   Chloroplast psbB Operon.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF170381; AAD56794.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1379 MW;  2C31687A3B73A338 CRC64;

  Query Match             2.4%;  Score 25.5;  DB 8;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 7.3e+04;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        134 NAGKDTNG 141
              |:||| ||
Db          4 NSGKD-NG 10


RESULT 34
Q84F20
ID   Q84F20      PRELIMINARY;      PRT;     9 AA.
AC   Q84F20;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-amylase (Fragment).
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89034018; PubMed=2460441;
RA   Nakamura K., Itoh Y., Yamane K.;
RT   "Enhanced secretion of beta-lactamase on structural modification of
RT   the Bacillus subtilis alpha-amylase signal peptide.";
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RL   J. Biochem. 104:265-269(1988).
DR   EMBL; D13786; BAC56113.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  728 MW;  C6B9BDDDDDC7687D CRC64;

  Query Match             2.3%;  Score 25;  DB 2;  Length 9;
  Best Local Similarity   71.4%;  Pred. No. 1e+06;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         19 LPGPSAA 25
              | ||:||
Db          1 LAGPAAA 7


RESULT 35
Q85G96
ID   Q85G96      PRELIMINARY;      PRT;     9 AA.
AC   Q85G96;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   AtpB (Fragment).
GN   ATPB.
OS   Pyrrhobryum mnioides.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC   Bryopsida; Bryidae; Rhizogoniales; Rhizogoniaceae; Pyrrhobryum.
OX   NCBI_TaxID=129293;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22569835; PubMed=12683518;
RA   McDaniel S.F., Shaw A.J.;
RT   "Phylogeographic structure and cryptic speciation in the trans-
RT   Antarctic moss Pyrrhobryum mnioides.";
RL   Evolution 57:205-215(2003).
DR   EMBL; AY143022; AAN52447.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1042 MW;  4040D1B415BAB1A3 CRC64;

  Query Match             2.3%;  Score 25;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        178 KTDSR 182
              |||||
Db          2 KTDSR 6


RESULT 36
Q8SAC2
ID   Q8SAC2      PRELIMINARY;      PRT;     10 AA.
AC   Q8SAC2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   AtpB (Fragment).
OS   Amblystegium varium.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC   Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX   NCBI_TaxID=111436;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AVaa;
RA   Vanderpoorten A., Shaw A.J., Cox C.J.;
RT   "Reconciled gene trees, molecular evolution, and species relationships
RT   in Amblystegium (Bryopsida).";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF464972; AAL75469.1; -.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1143 MW;  9D5040D1B415BAB1 CRC64;

  Query Match             2.3%;  Score 25;  DB 10;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        178 KTDSR 182
              |||||
Db          2 KTDSR 6


RESULT 37
Q47606
ID   Q47606      PRELIMINARY;      PRT;     11 AA.
AC   Q47606;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   REase protein (Fragment).
GN   REASE.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91139577; PubMed=1995588;
RA   Tao T., Bourne J.C., Blumenthal R.M.;
RT   "A family of regulatory genes associated with type II restriction-
RT   modification systems.";
RL   J. Bacteriol. 173:1367-1375(1991).
DR   EMBL; M63622; AAA24562.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1370 MW;  68C1FF9959CB133B CRC64;

  Query Match             2.3%;  Score 25;  DB 2;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 6.5e+04;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        197 IEVEKPF 203
              :|||| |
Db          1 MEVEKEF 7


RESULT 38
Q9C057
ID   Q9C057      PRELIMINARY;      PRT;     11 AA.
AC   Q9C057;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   HEX (Fragment).
GN   HEX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;
RT   "Human Hex 5'-flanking sequence.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF182950; AAK12833.1; -.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1125 MW;  2644D7FE686761F7 CRC64;

  Query Match             2.3%;  Score 25;  DB 4;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 6.5e+04;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         20 PGPSA 24
              |||:|
Db          6 PGPAA 10
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RESULT 39
Q9BQQ1
ID   Q9BQQ1      PRELIMINARY;      PRT;    12 AA.
AC   Q9BQQ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   BA28009.2.2 (Novel protein (Isoform 3)) (Fragment).
GN   DJ631M13.5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lloyd D.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL121582; CAC36069.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1017 MW;  4789B7218E787877 CRC64;

  Query Match             2.3%;  Score 25;  DB 4;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 7.3e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        104 GTGGKS 109
              | ||||
Db          7 GGGGKS 12


RESULT 40
Q9XNR6
ID   Q9XNR6      PRELIMINARY;      PRT;    12 AA.
AC   Q9XNR6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
GN   NAD3.
OS   Pylaiella littoralis.
OG   Mitochondrion.
OC   Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC   Acinetosporaceae; Pylaiella.
OX   NCBI_TaxID=2885;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=roscoff;
RX   MEDLINE=99346148; PubMed=10415341;
RA   Oudot M.P., Kloareg B., Loiseaux-de Goer S.;
RT   "The mitochondrial Pylaiella littoralis nad11 gene contains only the
RT   N-terminal FeS-binding domain.";
RL   Gene 235:131-137(1999).
DR   EMBL; AF110139; AAD44051.1; -.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion; Ubiquinone.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1501 MW;  49750746424B5B13 CRC64;

  Query Match             2.3%;  Score 25;  DB 8;  Length 12;
  Best Local Similarity   45.5%;  Pred. No. 7.3e+04;
  Matches    5;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        120 FKLKHYGPGWV 130
              | || | |   :
Db          2 FLLKEYYPALI 12


RESULT 41
Q8H6E6
ID   Q8H6E6      PRELIMINARY;      PRT;    12 AA.
AC   Q8H6E6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ENOD40-like protein.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Orthega;
RA   Larsen K.;
RT   "ENOD40 homologue from barley (Hordeum vulgare).";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF542513; AAN28683.1; -.
SQ   SEQUENCE   12 AA;  1367 MW;  3EEABFA918EB1733 CRC64;

  Query Match             2.3%;  Score 25;  DB 10;  Length 12;
  Best Local Similarity   57.1%;  Pred. No. 7.3e+04;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        152 AWLDGKH 158
              |||:  |
Db          4 AWLEHLH 10


RESULT 42
Q80IG7
ID   Q80IG7      PRELIMINARY;      PRT;    12 AA.
AC   Q80IG7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mini-cistron protein.
OS   Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV).
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC   Nucleopolyhedrovirus.
OX   NCBI_TaxID=208973;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Carstens E.B.;
RT   "Identification and analysis of the CfMNPV P143 gene.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF127530; AAF36457.1; -.
SQ   SEQUENCE   12 AA;  1252 MW;  C878D87A88B2CDD9 CRC64;

  Query Match             2.3%;  Score 25;  DB 12;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 7.3e+04;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         55 GLFGKTVPKT 64
              | |  | |:|
Db          3 GGFAVTTPRT 12


RESULT 43
Q7ZZN7
ID   Q7ZZN7      PRELIMINARY;      PRT;    13 AA.
AC   Q7ZZN7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Zinc finger protein (Fragment).
GN   ZIC3.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RA   Weber J.R., Sokol S.Y.;
```

```
RT   "Identification of a phylogenetically conserved activin-responsive
RT   enhancer in the Zic3 gene.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF506277; AAP20808.1; -.
FT   NON_TER       1      1
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1569 MW;  819B7A159F531861 CRC64;

  Query Match             2.3%;  Score 25;  DB 13;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 8e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         73 TGEKGF 78
              |||| |
Db          6 TGEKPF 11


RESULT 44
Q98YM1
ID   Q98YM1      PRELIMINARY;      PRT;    13 AA.
AC   Q98YM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Truncated pol protein (Fragment).
GN   POL.
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11676;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=991043;
RA   Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
RA   Korn K.;
RT   "Recovery of HIV-1 pol gene sequences by direct sequencing of
RT   amplification products derived from plasma samples.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF347446; AAK32523.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   13 AA;  1390 MW;  805408704623D1AA CRC64;

  Query Match             2.3%;  Score 25;  DB 15;  Length 13;
  Best Local Similarity   38.5%;  Pred. No. 8e+04;
  Matches    5;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        178 KTDSRDKPLKDVI 190
              :| : |   |:|:|
Db          1 ETGADDTVLEDII 13


RESULT 45
Q99PB8
ID   Q99PB8      PRELIMINARY;      PRT;    14 AA.
AC   Q99PB8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Adenosine kinase (EC 2.7.1.20) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Singh B., Lin A., Wu Z.-C., Gupta R.S.;
RT   "Gene Structure for Adenosine Kinase in Chinese Hamster and Human:
RT   High Frequency Mutants of CHO cells involve deletions of several
RT   introns and exons.";
RL   DNA Cell Biol. 0:0-0(2001).
DR   EMBL; AF318953; AAK07186.1; -.
DR   GO; GO:0004001; F:adenosine kinase activity; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Kinase; Transferase.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1526 MW;  27863376667D5A27 CRC64;

  Query Match             2.3%;  Score 25;  DB 11;  Length 14;
  Best Local Similarity   63.6%;  Pred. No. 8.8e+04;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    2;  Gaps    1;

Qy         23 SAADEKKKGPK 33
              :|||| |  ||
Db          2 AAADEPK--PK 10


Search completed: August 30, 2004, 10:55:31
Job time : 201.27 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 35.8378 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	3.7	14	1	EFTU_CANFA	P54835 canis famil
2	30	2.8	10	1	PAP1_PARMA	P81863 pardachirus
3	30	2.8	11	1	CA31_LITCI	P82089 litoria cit
4	30	2.8	13	1	GER2_HORVU	P28526 hordeum vul
5	29	2.7	11	1	CA32_LITCI	P82090 litoria cit
6	29	2.7	13	1	GER1_HORVU	P28525 hordeum vul
7	29	2.7	14	1	TAT_HV1W2	P12509 human immun
8	29	2.7	14	1	TAT_HV1Z8	P12511 human immun
9	28	2.6	8	1	RPCH_PANBO	P08939 pandalus bo
10	28	2.6	10	1	HTF_NAUCI	P10939 nauphoeta c
11	28	2.6	13	1	LPAA_PORGI	P81411 porphyromon
12	27	2.5	9	1	AL11_CARMA	P81814 carcinus ma
13	27	2.5	10	1	GONL_SQUAC	P27429 squalus aca
14	27	2.5	13	1	CRBL_VESMA	P17232 vespa manda
15	27	2.5	13	1	CRBL_VESTR	P17231 vespa tropi
16	27	2.5	13	1	TEMF_RANTE	P56921 rana tempor
17	26.5	2.4	12	1	TKN_KASSE	P08611 kassina sen
18	26	2.4	10	1	GON2_CHICK	P37043 gallus gall
19	26	2.4	10	1	GON3_ONCKE	P20367 oncorhynchu
20	26	2.4	12	1	FIF1_SARBU	P83349 sarcophaga
21	26	2.4	13	1	TEMA_RANTE	P56917 rana tempor
22	26	2.4	14	1	CRBL_VESOR	P17236 vespa orien
23	26	2.4	14	1	FIBB_MANLE	P14474 mandrillus
24	25	2.3	8	1	AKH_MELML	P25423 melolontha
25	25	2.3	8	1	AKH_TABAT	P14595 tabanus atr
26	25	2.3	10	1	HTF_TABAT	P14596 tabanus atr
27	25	2.3	10	1	SLAP_BACTG	P49325 bacillus th
28	25	2.3	11	1	RS30_ONCMY	P83328 oncorhynchu
29	25	2.3	12	1	HS9A_RAT	P82995 rattus norv
30	24.5	2.3	13	1	TA13_TREME	P01370 tremella me
31	24	2.2	10	1	BRK_ONCMY	Q9prz1 oncorhynchu
32	24	2.2	10	1	CAER_LITXA	P56264 litoria xan
33	24	2.2	10	1	TKS1_AEDAE	P42634 aedes aegyp
34	24	2.2	10	1	TKS2_AEDAE	P42635 aedes aegyp
35	24	2.2	13	1	HPB9_RANES	P32416 rana escule
36	23.5	2.2	12	1	RF1_CONSP	P58805 conus spuri
37	23.5	2.2	14	1	UN46_CLOPA	P81362 clostridium
38	23	2.1	8	1	LMT2_LOCMI	P22396 locusta mig
39	23	2.1	10	1	COXO_RAT	P80432 rattus norv
40	23	2.1	10	1	COXO_THUOB	P80982 thunnus obe
41	23	2.1	10	1	URA7_HUMAN	P34990 homo sapien
42	23	2.1	11	1	CORZ_PERAM	P11496 periplaneta
43	23	2.1	11	1	TKN4_PSEGU	P42989 pseudophryn
44	23	2.1	13	1	ADFB_TENMO	P83109 tenebrio mo
45	23	2.1	14	1	MAST_VESCR	P01516 vespa crabr

ALIGNMENTS

RESULT 1
EFTU_CANFA
ID EFTU_CANFA STANDARD; PRT; 14 AA.
AC P54835;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor Tu, mitochondrial (EF-Tu) (Fragment).
GN TUFM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: This protein promotes the GTP-dependent binding of
CC aminoacyl-tRNA to the A-site of ribosomes during protein
CC biosynthesis.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-Tu/EF-1A subfamily.
DR HSC-2DPAGE; P54835; DOG.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1600 MW; 8CAF0B6AE7CCDE41 CRC64;

Query Match 3.7%; Score 40; DB 1; Length 14;
Best Local Similarity 61.5%; Pred. No. 8.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy        174 VESTKTDSRDKPL 186
              ||: ||  ||||:
Db          2 VEAXKTYVRDKPI 14
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RESULT 2
PAP1_PARMA
ID PAP1_PARMA STANDARD; PRT; 10 AA.
AC P81863;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin I (PXI) (Fragment).
OS Pardachirus marmoratus (Red sea moses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.

```
OX   NCBI_TaxID=31087;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=87057369; PubMed=3782138;
RA   Lazarovici P., Primor N., Loew L.M.;
RT   "Purification and pore-forming activity of two hydrophobic
RT   polypeptides from the secretion of the Red sea moses sole (Pardachirus
RT   marmoratus).";
RL   J. Biol. Chem. 261:16704-16713(1986).
CC   -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC       properties. Forms voltage-dependent, ion-permeable channels in
CC       membranes. At high concentration causes cell membrane lysis. Shown
CC       to be 5-10 times more toxic, cytolytic and active in membrane pore
CC       formation than pardaxin II.
CC   -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pardaxin family.
KW   Toxin.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1063 MW;  D399C36760572DD9 CRC64;

  Query Match             2.8%;  Score 30;  DB 1;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 4.6e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         15 FFLLLPG 21
              || |:||
Db          2 FFALIPG 8


RESULT 3
CA31_LITCI
ID   CA31_LITCI     STANDARD;      PRT;    11 AA.
AC   P82089;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Caerulein 3.1/3.1Y4.
OS   Litoria citropa (Australian blue mountains tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=94770;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=20057701; PubMed=10589099;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT   "Caerulein-like peptides from the skin glands of the Australian blue
RT   montains tree frog Litoria citropa. Part 1. Sequence determination
RT   using electrospray mass spectrometry.";
RL   Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC   -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC   -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC       sulfated.
CC   -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC   -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW   Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       4      4       SULFATION.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1347 MW;  10DAB7D67861A86B CRC64;

  Query Match             2.8%;  Score 30;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 5.1e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         125 YGPGWV 130
               || ||:
Db           4 YGTGWM 9


RESULT 4
GER2_HORVU
ID   GER2_HORVU     STANDARD;      PRT;    13 AA.
AC   P28526;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Germin GS2 (Fragment).
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=cv. CM 72; TISSUE=Root;
RA   Hurkman W.J., Tao H.P., Tanaka C.K.;
RT   "Germin-like polypeptides increase in barley roots during salt
RT   stress.";
RL   Plant Physiol. 97:366-374(1991).
CC   -!- FUNCTION: May play a role in altering the properties of cell walls
CC       during germinative growth.
CC   -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.
CC   -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the
CC       mature region, but not in the tip. Not detected in leaves.
CC   -!- INDUCTION: Increased by salt stress in roots and decreased by salt
CC       stress in coleoptile.
CC   -!- PTM: Glycosylated.
CC   -!- SIMILARITY: Belongs to the germin family.
DR   InterPro; IPR001929; Germin.
DR   PROSITE; PS00725; GERMIN; PARTIAL.
KW   Apoplast; Cell wall; Glycoprotein; Multigene family.
FT   UNSURE       10     10
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1484 MW;  43FB4A1AA3B7B6D7 CRC64;

  Query Match             2.8%;  Score 30;  DB 1;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 6.1e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         185 PLKDVIIAD 193
               ||:|  |||
Db           5 PLQDFCIAD 13


RESULT 5
CA32_LITCI
ID   CA32_LITCI     STANDARD;      PRT;    11 AA.
AC   P82090;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Caerulein 3.2/3.2Y4.
OS   Litoria citropa (Australian blue mountains tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=94770;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=20057701; PubMed=10589099;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT   "Caerulein-like peptides from the skin glands of the Australian blue
RT   montains tree frog Litoria citropa. Part 1. Sequence determination
RT   using electrospray mass spectrometry.";
```

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RL   Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC   -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC   -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC       sulfated.
CC   -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC   -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW   Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       4      4       SULFATION.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1363 MW;  10DAB8867861A86B CRC64;

  Query Match              2.7%;  Score 29;  DB 1;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 6.2e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        125 YGPGW 129
              || ||
Db          4 YGTGW 8


RESULT 6
GER1_HORVU
ID   GER1_HORVU     STANDARD;      PRT;    13 AA.
AC   P28525;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Germin GS1 (Fragment).
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=cv. CM 72; TISSUE=Root;
RA   Hurkman W.J., Tao H.P., Tanaka C.K.;
RT   "Germin-like polypeptides increase in barley roots during salt
RT   stress.";
RL   Plant Physiol. 97:366-374(1991).
CC   -!- FUNCTION: May play a role in altering the properties of cell
CC       walls during germinative growth.
CC   -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.
CC   -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in
CC       the mature region, but not in the tip. Not detected in leaves.
CC   -!- INDUCTION: Increased by salt stress in roots and decreased by salt
CC       stress in coleoptile.
CC   -!- PTM: Glycosylated.
CC   -!- SIMILARITY: Belongs to the germin family.
DR   InterPro; IPR001929; Germin.
DR   PROSITE; PS00725; GERMIN; PARTIAL.
KW   Apoplast; Cell wall; Glycoprotein; Multigene family.
FT   UNSURE       10     10
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1470 MW;  43FB588AA3B7B6D7 CRC64;

  Query Match              2.7%;  Score 29;  DB 1;  Length 13;
  Best Local Similarity   55.6%;  Pred. No. 7.4e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        185 PLKDVIIAD 193
              ||:|  :||
Db          5 PLQDFCVAD 13


RESULT 7
TAT_HV1W2
ID   TAT_HV1W2      STANDARD;      PRT;    14 AA.
AC   P12509;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   TAT protein (Transactivating regulatory protein) (Fragment).
GN   TAT.
OS   Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11705;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86235450; PubMed=3012778;
RA   Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA   Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT   "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT   at risk for AIDS.";
RL   Science 232:1548-1553(1986).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter.
CC   -!- SUBUNIT: Binds cyclin T1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC   -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC       BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC       WAS PERINATALLY INFECTED BY HER MOTHER.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M12507; AAB12991.1; -.
DR   HIV; M12507; TAT$WMJ2.
KW   Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW   AIDS.
FT   NON_TER       1      1
SQ   SEQUENCE   14 AA;  1467 MW;  37CC737BFEF67AA8 CRC64;

  Query Match              2.7%;  Score 29;  DB 1;  Length 14;
  Best Local Similarity   75.0%;  Pred. No. 8.1e+03;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        101 RGDGTGGK 108
              ||| || |
Db          6 RGDPTGPK 13


RESULT 8
TAT_HV1Z8
ID   TAT_HV1Z8      STANDARD;      PRT;    14 AA.
AC   P12511;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   TAT protein (Transactivating regulatory protein) (Fragment).
GN   TAT.
OS   Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX   NCBI_TaxID=11681;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88281278; PubMed=3395517;
RA   Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA   Gallo R.C.;
RT   "Nucleotide sequence analysis of the env gene of a new Zairian
RT   isolate of HIV-1.";
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RL   AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC   -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC       trans-activating responsive sequence (TAR) RNA element and
CC       activates transcription initiation and/or elongation from the LTR
CC       promoter.
CC   -!- SUBUNIT: Binds cyclin T1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC   -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC       ZAIREAN MALE.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J03653; AAA44685.1; -.
DR   HIV; J03653; TAT$JY1.
KW   Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW   AIDS.
FT   NON_TER       1      1
SQ   SEQUENCE   14 AA;  1453 MW;  37CC737BF82D7AA8 CRC64;

  Query Match             2.7%;  Score 29;  DB 1;  Length 14;
  Best Local Similarity   75.0%;  Pred. No. 8.1e+03;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        101 RGDGTGGK 108
              ||| || |
Db          6 RGDPTGPK 13


RESULT 9
RPCH_PANBO
ID   RPCH_PANBO     STANDARD;      PRT;     8 AA.
AC   P08939;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Red pigment concentrating hormone (RPCH).
OS   Pandalus borealis (Northern red shrimp).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC   Pandalidae; Pandalus.
OX   NCBI_TaxID=6703;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75054965; PubMed=4433569;
RA   Fernlund P.;
RT   "Structure of the red-pigment-concentrating hormone of the shrimp,
RT   Pandalus borealis.";
RL   Biochim. Biophys. Acta 371:304-311(1974).
CC   -!- FUNCTION: This hormone adapts the animal to light backgrounds by
CC       stimulating concentration of the pigment of its red body-
CC       chromatophores.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; A61348; A61348.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  948 MW;  86786775B9C44736 CRC64;

  Query Match             2.6%;  Score 28;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        124 HYGPGW 129
              :: |||
Db          3 NFSPGW 8


RESULT 10
HTF_NAUCI
ID   HTF_NAUCI      STANDARD;      PRT;    10 AA.
AC   P10939;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).
OS   Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS   Leucophaea maderae (Madeira cockroach),
OS   Blattella germanica (German cockroach), and
OS   Gromphadorina portentosa (Madagascan hissing cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Nauphoeta.
OX   NCBI_TaxID=6990, 6988, 6973, 36953;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
RX   MEDLINE=87100208; PubMed=3801028;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
RT   corpus cardiacum of the cockroach, Nauphoeta cinerea.";
RL   Biochem. Biophys. Res. Commun. 141:774-781(1986).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.maderae, G.portentosa, and B.germanica;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=B.germanica;
RX   MEDLINE=91179584; PubMed=2080017;
RA   Veenstra J.A., Camps F.;
RT   "Structure of the hypertrehalosemic neuropeptide of the German
RT   cockroach, Blattella germanica.";
RL   Neuropeptides 15:107-109(1990).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; A26381; A26381.
DR   PIR; A60421; A60421.
DR   PIR; S08997; S08997.
DR   PIR; S08998; S08998.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1092 MW;  056236786775B9C4 CRC64;

  Query Match             2.6%;  Score 28;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 6.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        124 HYGPGW 129
              :: |||
Db          3 NFSPGW 8


RESULT 11
LPAA_PORGI
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ID   LPAA_PORGI     STANDARD;      PRT;    13 AA.
AC   P81411;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Lipid-A-associated protein (Fragment).
OS   Porphyromonas gingivalis (Bacteroides gingivalis).
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Porphyromonadaceae; Porphyromonas.
OX   NCBI_TaxID=837;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W50;
RX   MEDLINE=99061194; PubMed=9846737;
RA   Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
RA   Curtis M., Henderson B., Tabona P.;
RT   "A lipid A-associated protein of Porphyromonas gingivalis, derived
RT   from the haemagglutinating domain of the RI protease gene family, is
RT   a potent stimulator of interleukin 6 synthesis.";
RL   Microbiology 144:3019-3026(1998).
CC   -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
CC       THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
CC       CELL.
FT   VARIANT      12     12       G -> F.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1346 MW;  38EA796EAFA63AB7 CRC64;

  Query Match             2.6%;  Score 28;  DB 1;  Length 13;
  Best Local Similarity   55.6%;  Pred. No. 9.1e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        134 NAGKDTNGS 142
              |  |||:|:
Db          5 NPDKDTDGN 13


RESULT 12
AL11_CARMA
ID   AL11_CARMA     STANDARD;      PRT;     9 AA.
AC   P81814;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 11.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       9      9       AMIDATION.
SQ   SEQUENCE   9 AA;  927 MW;  832D79CDCB46D861 CRC64;

  Query Match             2.5%;  Score 27;  DB 1;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         72 ATGEKGFG 79
              |||:  ||
Db          1 ATGQYAFG 8


RESULT 13
GONL_SQUAC
ID   GONL_SQUAC     STANDARD;      PRT;    10 AA.
AC   P27429;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH)
DE   (Luliberin).
OS   Squalus acanthias (Spiny dogfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92335300; PubMed=1631133;
RA   Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA   Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT   "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
RT   dogfish brain provides insight into GnRH evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC   -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GnRH family.
DR   PIR; A46030; A46030.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1204 MW;  284B32337871F5A3 CRC64;

  Query Match             2.5%;  Score 27;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 8.4e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        123 KHYGPGWV 130
              :|:  ||:
Db          1 QHWSHGWL 8


RESULT 14
CRBL_VESMA
ID   CRBL_VESMA     STANDARD;      PRT;    13 AA.
AC   P17232;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vespid chemotactic peptide M (VESCP-M).
OS   Vespa mandarinia (Hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7446;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA   Fujino M.;
RL   (In) Munekata E. (eds.);
RL   Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL   Osaka (1984).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1384 MW;  2650402B9DF92338 CRC64;

  Query Match             2.5%;  Score 27;  DB 1;  Length 13;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy        160 VFGKVLEGM 168
              : ||:| |:
Db          4 IIGKLLSGL 12


RESULT 15
CRBL_VESTR
ID   CRBL_VESTR     STANDARD;      PRT;    13 AA.
AC   P17231;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Vespid chemotactic peptide T (VESCP-T).
OS   Vespa tropica (Hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7450;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Yasuhara T., Nakajima T., Erspaer V.;
RL   (In) Sakakibara S. (eds.);
RL   Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL   Osaka (1983).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1354 MW;  220140365DFE5338 CRC64;

  Query Match             2.5%;  Score 27;  DB 1;  Length 13;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 VFGKVLEGM 168
              : ||:| |:
Db          4 ILGKILGGL 12


RESULT 16
TEMF_RANTE
ID   TEMF_RANTE     STANDARD;      PRT;    13 AA.
AC   P56921;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Temporin F.
OS   Rana temporaria (European common frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8407;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97175050; PubMed=9022710;
RA   Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA   Barra D.;
RT   "Temporins, antimicrobial peptides from the European red frog Rana
RT   temporaria.";
RL   Eur. J. Biochem. 242:788-792(1996).
CC   -!- FUNCTION: Has antibacterial activity against Gram-negative and
CC       Gram-positive bacteria.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the brevinin family.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1370 MW;  2653612B9DECC338 CRC64;

  Query Match             2.5%;  Score 27;  DB 1;  Length 13;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+04;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        160 VFGKVLEGM 168
              : ||:| |:
Db          4 LIGKVLSGI 12


RESULT 17
TKN_KASSE
ID   TKN_KASSE      STANDARD;      PRT;    12 AA.
AC   P08611;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Kassinin.
OS   Kassina senegalensis (Senegal running frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
OC   Kassina.
OX   NCBI_TaxID=8415;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=77246385; PubMed=891753;
RA   Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
RT   "Amino acid composition and sequence of kassinin, a tachykinin
RT   dodecapeptide from the skin of the African frog Kassina
RT   senegalensis.";
RL   Experientia 33:857-858(1977).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; S07206; S07206.
DR   PDB; 1MYU; 16-OCT-02.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW   3D-structure.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1336 MW;  91757AB89DD6DAB5 CRC64;

  Query Match             2.4%;  Score 26.5;  DB 1;  Length 12;
  Best Local Similarity   63.6%;  Pred. No. 1.1e+04;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         61 VPKTVDNFVAL 71
              |||: | || |
Db          2 VPKS-DQFVGL 11


RESULT 18
GON2_CHICK
ID   GON2_CHICK     STANDARD;      PRT;    10 AA.
AC   P37043; P20408; P81750;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
DE   (LH-RH II) (Luliberin II).
OS   Gallus gallus (Chicken),
OS   Alligator mississippiensis (American alligator),
OS   Squalus acanthias (Spiny dogfish),
OS   Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and
OS   Clupea pallasii (Pacific herring).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
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RN   [1]
RP   SEQUENCE.
RC   SPECIES=Chicken; TISSUE=Hypothalamus;
RX   MEDLINE=84222059; PubMed=6427779;
RA   Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA   Matsuo H.;
RT   "Identification of the second gonadotropin-releasing hormone in
RT   chicken hypothalamus: evidence that gonadotropin secretion is
RT   probably controlled by two distinct gonadotropin-releasing hormones
RT   in avian species.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=A.mississippiensis; TISSUE=Brain;
RX   MEDLINE=91352338; PubMed=1882082;
RA   Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA   Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT   "Primary structure of two forms of gonadotropin-releasing hormone
RT   from brains of the American alligator (Alligator mississippiensis).";
RL   Regul. Pept. 33:105-116(1991).
RN   [3]
RP   SEQUENCE.
RC   SPECIES=S.acanthias; TISSUE=Brain;
RX   MEDLINE=92335300; PubMed=1631133;
RA   Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA   Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT   "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
RT   dogfish brain provides insight into GnRH evolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
RN   [4]
RP   SEQUENCE.
RC   SPECIES=H.colliei; TISSUE=Brain;
RX   MEDLINE=91340067; PubMed=1678723;
RA   Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA   Lee T.;
RT   "Primary structure of gonadotropin-releasing hormone from the brain
RT   of a holocephalan (ratfish: Hydrolagus colliei).";
RL   Gen. Comp. Endocrinol. 82:152-161(1991).
RN   [5]
RP   SEQUENCE, AND FUNCTION.
RC   SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX   MEDLINE=20114351; PubMed=10650929;
RA   Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA   Chang J.P., Rivier J.E., Sherwood N.M.;
RT   "Primary structure and function of three gonadotropin-releasing
RT   hormones, including a novel form, from an ancient teleost, herring.";
RL   Endocrinology 141:505-512(2000).
CC   -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GnRH family.
DR   PIR; A61126; A61126.
DR   PIR; B46030; B46030.
DR   PIR; B60066; RHAQ2.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1254 MW;  284B2E437871F5A3 CRC64;

  Query Match              2.4%;  Score 26;  DB 1;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 1e+04;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        123 KHYGPGW 129
              :|:  ||
Db          1 QHWSHGW 7


RESULT 19
GON3_ONCKE
ID   GON3_ONCKE     STANDARD;      PRT;     10 AA.
AC   P20367; P81751;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
DE   RH III) (Luliberin III).
GN   GNRH3.
OS   Oncorhynchus keta (Chum salmon), and
OS   Clupea pallasii (Pacific herring).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8018, 30724;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=O.keta;
RX   MEDLINE=83195140; PubMed=6341999;
RA   Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT   "Characterization of a teleost gonadotropin-releasing hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN   [2]
RP   SEQUENCE, AND FUNCTION.
RC   SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX   MEDLINE=20114351; PubMed=10650929;
RA   Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA   Chang J.P., Rivier J.E., Sherwood N.M.;
RT   "Primary structure and function of three gonadotropin-releasing
RT   hormones, including a novel form, from an ancient teleost, herring.";
RL   Endocrinology 141:505-512(2000).
CC   -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC       the secretion of both luteinizing and follicle-stimulating
CC       hormones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GnRH family.
DR   PIR; A21114; A21114.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1230 MW;  284B3233786B45A3 CRC64;

  Query Match              2.4%;  Score 26;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 1e+04;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        123 KHYGPGWV 130
              :|:  ||:
Db          1 QHWSYGWL 8


RESULT 20
FIF1_SARBU
ID   FIF1_SARBU     STANDARD;      PRT;     12 AA.
AC   P83349;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Neb-FIRFamide 1.
OS   Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC   Sarcophagidae; Sarcophaga.
OX   NCBI_TaxID=7385;
RN   [1]
RP   SEQUENCE, AMIDATION, AND FUNCTION.
RC   TISSUE=CNS;
RX   MEDLINE=22342733; PubMed=12438685;
RA   Meeusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA   Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT   "Identification in Drosophila melanogaster of the invertebrate G
RT   protein-coupled FMRFamide receptor.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC   -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC       junctions.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neuropeptide; Amidation.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1389 MW;  2DC45519C14AB5A7 CRC64;

  Query Match             2.4%;  Score 26;  DB 1;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+04;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         62 PKTVDNFV 69
              |:  |||:
Db          3 PQPSDNFI 10


RESULT 21
TEMA_RANTE
ID   TEMA_RANTE     STANDARD;      PRT;    13 AA.
AC   P56917;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Temporin A.
OS   Rana temporaria (European common frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8407;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97175050; PubMed=9022710;
RA   Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA   Barra D.;
RT   "Temporins, antimicrobial peptides from the European red frog Rana
RT   temporaria.";
RL   Eur. J. Biochem. 242:788-792(1996).
CC   -!- FUNCTION: Has antibacterial activity against Gram-positive
CC       bacteria.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the brevinin family.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES      13     13       AMIDATION.
SQ   SEQUENCE   13 AA;  1398 MW;  2653612B9DECD408 CRC64;

  Query Match             2.4%;  Score 26;  DB 1;  Length 13;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+04;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         49 VGRVIFGL 56
              :|||: |:
Db          5 IGRVLSGI 12


RESULT 22
CRBL_VESOR
ID   CRBL_VESOR     STANDARD;      PRT;    14 AA.
AC   P17236;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Histamine releasing peptide II (HR-II).
OS   Vespa orientalis (Oriental hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7447;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RA   Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA   Rozynov B.V., Gushchin I.S.;
RT   "Structure and properties of histamine releasing peptides from the
RT   venom of Vespa orientalis hornet.";
RL   Bioorg. Khim. 7:1467-1477(1981).
CC   -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC       of neutrophils.
DR   PIR; JN0390; JN0390.
KW   Mast cell degranulation; Chemotaxis; Amidation.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1524 MW;  22015B4A6CEDFD38 CRC64;

  Query Match             2.4%;  Score 26;  DB 1;  Length 14;
  Best Local Similarity   30.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 VVFGKVLEGM 168
              :: ||:::|:
Db          4 LILGKLVKGL 13


RESULT 23
FIBB_MANLE
ID   FIBB_MANLE     STANDARD;      PRT;    14 AA.
AC   P14474;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN   FGB.
OS   Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Mandrillus.
OX   NCBI_TaxID=9568;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69115139; PubMed=4974768;
RA   Doolittle R.F., Glascow C., Mross G.A.;
RT   "Characterization of fibrinopeptides A and B from a drill (Mandrillus
RT   leucophaeus).";
RL   Biochim. Biophys. Acta 175:217-219(1969).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Plasma; Pyrrolidone carboxylic acid.
FT   PEPTIDE      1     14       FIBRINOPEPTIDE B.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   NON_TER     14     14
SQ   SEQUENCE   14 AA;  1434 MW;  6695B0F11EF72E1B CRC64;

  Query Match             2.4%;  Score 26;  DB 1;  Length 14;
  Best Local Similarity   42.9%;  Pred. No. 1.5e+04;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    6;  Gaps    1;

Qy         45 GDEDVGRVIFGLFG 58
              |:|:      ||||
Db          5 GBEE------GLFG 12


RESULT 24
AKH_MELML
ID   AKH_MELML      STANDARD;      PRT;     8 AA.
AC   P25423;
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DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Adipokinetic hormone (AKH).
OS   Melolontha melolontha (Cockchafer),
OS   Geotrupes stercorosus (Dor beetle), and
OS   Pachnoda marginata (Flower beetle).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
OC   Scarabaeidae; Melolonthinae; Melolontha.
OX   NCBI_TaxID=7061, 7087, 7058;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=91248100; PubMed=2039445;
RA   Gaede G.;
RT   "A unique charged tyrosine-containing member of the adipokinetic
RT   hormone/red-pigment-concentrating hormone peptide family isolated and
RT   sequenced from two beetle species.";
RL   Biochem. J. 275:671-677(1991).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=P.marginata; TISSUE=Corpora cardiaca;
RX   MEDLINE=92265187; PubMed=1586453;
RA   Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
RT   "Primary structures of neuropeptides isolated from the corpora
RT   cardiaca of various cetonid beetle species determined by
RT   pulsed-liquid phase sequencing and tandem fast atom bombardment mass
RT   spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 373:133-142(1992).
CC   -!- FUNCTION: This hormone, released from cells in the corpora
CC       cardiaca after the beginning of flight, causes release of
CC       diglycerides from the fat body and then stimulates the flight
CC       muscles to use these diglycerides as an energy source.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; A58641; A58641.
DR   PIR; S15422; S15422.
DR   PIR; S21663; S21663.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  1022 MW;  867AB775AB544736 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        124 HYGPGW 129
              :| | |
Db          3 NYSPDW 8


RESULT 25
AKH_TABAT
ID   AKH_TABAT      STANDARD;      PRT;     8 AA.
AC   P14595;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE   (DCC I).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC   Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: This hormone, released from cells in the corpora
CC       cardiaca after the beginning of flight, causes release of
CC       diglycerides from the fat body and then stimulates the flight
CC       muscles to use these diglycerides as an energy source.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; A33995; A33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  949 MW;  86786771A9D1A736 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        125 YGPGW 129
              : |||
Db          4 FTPGW 8


RESULT 26
HTF_TABAT
ID   HTF_TABAT      STANDARD;      PRT;     10 AA.
AC   P14596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE   (DCC II).
OS   Tabanus atratus (Horse fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC   Tabanus.
OX   NCBI_TaxID=7207;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90046758; PubMed=2813385;
RA   Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA   Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT   "Primary structure of two neuropeptide hormones with adipokinetic and
RT   hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT   flies (Diptera).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; B33995; B33995.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1169 MW;  916036786771A9D1 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.3e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        125 YGPGW 129
              : |||
Db          4 FTPGW 8
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RESULT 27
SLAP_BACTG
ID   SLAP_BACTG     STANDARD;      PRT;    10 AA.
AC   P49325;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   S-layer protein (Surface layer protein) (Fragment).
OS   Bacillus thuringiensis (subsp. galleriae).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=29338;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=NRRL 4045;
RX   MEDLINE=90078111; PubMed=2592346;
RA   Luckevich M.D., Beveridge T.J.;
RT   "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL   J. Bacteriol. 171:6656-6667(1989).
CC   -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC       of proteins which coat the surface of bacteria.
CC   -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC       S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR   PIR; A60476; A60476.
KW   Cell wall; S-layer.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1080 MW;  57AECACAB769D1A3 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+04;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        112 GERFPD 117
              |: |||
Db          2 GKTFPD 7


RESULT 28
RS30_ONCMY
ID   RS30_ONCMY     STANDARD;      PRT;    11 AA.
AC   P83328;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   40S ribosomal protein S30 (Fragment).
GN   FAU.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Skin mucus;
RX   MEDLINE=22142142; PubMed=12147245;
RA   Fernandes J.M.O., Smith V.J.;
RT   "A novel antimicrobial function for a ribosomal peptide from rainbow
RT   trout skin.";
RL   Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC   -!- FUNCTION: Has antibacterial activity against Gram-positive
CC       bacteria.
CC   -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC   -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW   Ribosomal protein; Antibiotic.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1123 MW;  2312AB630DD735B8 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+04;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        131 SMANAGK 137
              |:| |||
Db          5 SLARAGK 11


RESULT 29
HS9A_RAT
ID   HS9A_RAT       STANDARD;      PRT;    12 AA.
AC   P82995;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Heat shock protein HSP 90-alpha (Fragment).
GN   HSPCA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=21589773; PubMed=11732320;
RA   Langer T., Fasold H.;
RT   "Isolation and quantification of the heat shock protein 90 alpha and
RT   beta isoforms from rat liver.";
RL   Protoplasma 218:54-56(2001).
CC   -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
CC       similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the heat shock protein 90 family.
DR   InterPro; IPR001404; Hsp90.
DR   PROSITE; PS00298; HSP90; PARTIAL.
KW   Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT   MOD_RES       4      4       PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT                                SIMILARITY).
FT   MOD_RES       6      6       PHOSPHORYLATION (BY DS-DNA KINASE) (BY
FT                                SIMILARITY).
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1432 MW;  DE47C322CAB6C1B6 CRC64;

  Query Match             2.3%;  Score 25;  DB 1;  Length 12;
  Best Local Similarity   30.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        178 KTDSRDKPLK 187
              :| ::|:|::
Db          3 ETQTQDQPME 12


RESULT 30
TA13_TREME
ID   TA13_TREME     STANDARD;      PRT;    13 AA.
AC   P01370;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tremerogen A-13.
OS   Tremella mesenterica (Jelly fungus).
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
OX   NCBI_TaxID=5217;
RN   [1]
RP   SEQUENCE.
RA   Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
RT   "Peptide sex hormones inducing conjugation tube formation in
RT   compatible mating-type cells of Tremella mesenterica.";
RL   Science 212:1525-1527(1981).
CC   -!- FUNCTION: Tremerogen A-13 is produced by the a mating-type cells
CC       and induces formation of conjugation tubes in a mating-type cells.
DR   PIR; A01641; JTJG3.
KW   Lipoprotein; Prenylation; Pheromone.
FT   LIPID        13     13       S-farnesyl cysteine.
SQ   SEQUENCE   13 AA;  1204 MW;  680304A9697BA864 CRC64;
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  Query Match              2.3%;  Score 24.5;  DB 1;  Length 13;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+04;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         95 QGGDFTRGDGTG 106
              :||   ||| :|
Db          1 EGGG-NRGDPSG 11


RESULT 31
BRK_ONCMY
ID   BRK_ONCMY      STANDARD;      PRT;    10 AA.
AC   Q9PRZ1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lysyl-bradykinin-like.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94039817; PubMed=8224232;
RA   Conlon J.M., Olson K.R.;
RT   "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT   trout plasma.";
RL   FEBS Lett. 334:75-78(1993).
CC   -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC       THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Plasma.
CC   -!- SIMILARITY: Belongs to the bradykinin family.
DR   PIR; S39030; S39030.
KW   Bradykinin; Vasodilator.
SQ   SEQUENCE   10 AA;  1193 MW;  33C59075A3786777 CRC64;

  Query Match              2.2%;  Score 24;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         127 PGW 129
               |||
Db           4 PGW 6


RESULT 32
CAER_LITXA
ID   CAER_LITXA     STANDARD;      PRT;    10 AA.
AC   P56264;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Caerulein.
OS   Litoria xanthomera (Orange-thighed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=79697;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97374000; PubMed=9230483;
RA   Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA   Ramsay S.L.;
RT   "New caerin antibacterial peptides from the skin glands of the
RT   Australian tree frog Litoria xanthomera.";
RL   J. Pept. Sci. 3:181-185(1997).
CC   -!- FUNCTION: Hypotensive neuropeptide.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC   -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; 1.
KW   Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       4      4       SULFATION.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1290 MW;  99DBF3837861BB5A CRC64;

  Query Match              2.2%;  Score 24;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         151 TAWLD 155
               | |:|
Db           5 TGWMD 9


RESULT 33
TKS1_AEDAE
ID   TKS1_AEDAE     STANDARD;      PRT;    10 AA.
AC   P42634;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialokinin I.
OS   Aedes aegypti (Yellowfever mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX   NCBI_TaxID=7159;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Rockefeller; TISSUE=Salivary gland;
RX   MEDLINE=94105119; PubMed=8278354;
RA   Champagne D.E., Ribeiro J.M.C.;
RT   "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT   mosquito Aedes aegypti.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC   -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC       site of feeding.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; A49581; A49581.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1145 MW;  3DCFDE6B59C33AA8 CRC64;

  Query Match              2.2%;  Score 24;  DB 1;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 1.5e+04;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          73 TGEKGFG 79
               ||:| :|
Db           2 TGDKFYG 8


RESULT 34
TKS2_AEDAE
ID   TKS2_AEDAE     STANDARD;      PRT;    10 AA.
AC   P42635;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialokinin II.
OS   Aedes aegypti (Yellowfever mosquito).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX   NCBI_TaxID=7159;
RN   [1]
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RP   SEQUENCE.
RC   STRAIN=Rockefeller; TISSUE=Salivary gland;
RX   MEDLINE=94105119; PubMed=8278354;
RA   Champagne D.E., Ribeiro J.M.C.;
RT   "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT   mosquito Aedes aegypti.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC   -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC       site of feeding.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; B49581; B49581.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1146 MW;  3DC77C6B59C33AA8 CRC64;

  Query Match             2.2%;  Score 24;  DB 1;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 1.5e+04;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         73 TGEKGFG 79
              ||:| :|
Db          2 TGDKFYG 8


RESULT 35
HPB9_RANES
ID   HPB9_RANES     STANDARD;      PRT;    13 AA.
AC   P32416;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hemolytic protein B9 (Fragment).
OS   Rana esculenta (Edible frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8401;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90198965; PubMed=2317508;
RA   Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA   Barra D., Bossa F.;
RT   "Purification and characterization of bioactive peptides from skin
RT   extracts of Rana esculenta.";
RL   Biochim. Biophys. Acta 1033:318-323(1990).
CC   -!- FUNCTION: Shows hemolytic activity.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
DR   PIR; S09019; S09019.
KW   Amphibian defense peptide; Amidation; Hemolysis.
FT   MOD_RES      13     13       AMIDATION.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1402 MW;  C6B41A765DF9287D CRC64;

  Query Match             2.2%;  Score 24;  DB 1;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 2e+04;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         52 VIFGLFGK 59
              :| || ||
Db          4 LIAGLLGK 11


RESULT 36
RF1_CONSP
ID   RF1_CONSP      STANDARD;      PRT;    12 AA.
AC   P58805;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Conorfamide-Sr1.
OS   Conus spurius (Alphabet cone).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC   Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC   Neogastropoda; Conoidea; Conidae; Conus.
OX   NCBI_TaxID=192919;
RN   [1]
RP   SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC   TISSUE=Venom;
RX   MEDLINE=21605839; PubMed=11738233;
RA   Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA   Olivera B.M., Heimer de la Cotera E.P.;
RT   "Conorfamide, a Conus venom peptide belonging to the RFamide family of
RT   neuropeptides.";
RL   Toxicon 40:401-407(2002).
CC   -!- FUNCTION: Causes hyperactivity in mice.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC   -!- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
KW   Neurotoxin; Toxin; Amidation.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1456 MW;  2510671E49D772D3 CRC64;

  Query Match             2.2%;  Score 23.5;  DB 1;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        126 GP-GWV 130
              || |||
Db          1 GPMGWV 6


RESULT 37
UN46_CLOPA
ID   UN46_CLOPA     STANDARD;      PRT;    14 AA.
AC   P81362;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Unknown protein CP 46 from 2D-page (Fragment).
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC       PROTEIN IS: 5.4, ITS MW IS: 38.2 kDa.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1550 MW;  198078F4C0367170 CRC64;

  Query Match             2.2%;  Score 23.5;  DB 1;  Length 14;
  Best Local Similarity   38.5%;  Pred. No. 2.4e+04;
  Matches    5;  Conservative    5;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         38 VYFDLRIGDEDVG 50
              :: || ||: ::|
Db          2 IFNDL-IGNNNIG 13


RESULT 38
LMT2_LOCMI
ID   LMT2_LOCMI     STANDARD;      PRT;     8 AA.
AC   P22396;
DT   01-AUG-1991 (Rel. 19, Created)
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DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   Locustamyotropin 2 (LOM-MT-2).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT   "Isolation, identification and synthesis of locustamyotropin II, an
RT   additional neuropeptide of Locusta migratoria. Member of the
RT   cephalomyotropic peptide family.";
RL   Insect Biochem. 20:479-484(1990).
CC   -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC       activity).
CC   -!- SIMILARITY: Belongs to the pyrokinin family.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  26341771A9CAA87B CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         97 GDFT 100
              ||||
Db          2 GDFT 5


RESULT 39
COXO_RAT
ID   COXO_RAT       STANDARD;      PRT;    10 AA.
AC   P80432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
DE   (VIIIA) (Fragment).
GN   COX7C OR COX7C1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=Wistar; TISSUE=Heart, and Liver;
RX   MEDLINE=95324529; PubMed=7601105;
RA   Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT   "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT   amino-terminal sequences suggest identity of the fetal heart and the
RT   adult liver isoform.";
RL   Eur. J. Biochem. 230:235-241(1995).
CC   -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC       chains of cytochrome c oxidase, the terminal oxidase in
CC       mitochondrial electron transport.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR   PIR; S65388; S65388.
KW   Oxidoreductase; Mitochondrion.
FT   NON_TER       10      10
SQ   SEQUENCE   10 AA;  1117 MW;  126DE767687B1B0B CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy        124 HY--GPG 128
               ||  |||
Db          2 HYEEGPG 8


RESULT 40
COXO_THUOB
ID   COXO_THUOB      STANDARD;      PRT;    10 AA.
AC   P80982;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Cytochrome c oxidase polypeptide VIIc (EC 1.9.3.1) (Fragment).
OS   Thunnus obesus (Bigeye tuna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC   Scombridae; Thunnus.
OX   NCBI_TaxID=8241;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart, and Liver;
RX   MEDLINE=97454291; PubMed=9310366;
RA   Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA   Kadenbach B.;
RT   "The subunit structure of cytochrome-c oxidase from tuna heart and
RT   liver.";
RL   Eur. J. Biochem. 248:99-103(1997).
CC   -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC       chains of cytochrome c oxidase, the terminal oxidase in
CC       mitochondrial electron transport.
CC   -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC       c + 2 H(2)O.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC   -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR   PIR; S77990; S77990.
KW   Oxidoreductase; Inner membrane; Mitochondrion.
FT   NON_TER       10      10
SQ   SEQUENCE   10 AA;  1059 MW;  126DE767687B1DCB CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 10;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+04;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy        124 HY--GPG 128
               ||  |||
Db          2 HYAEGPG 8


RESULT 41
URA7_HUMAN
ID   URA7_HUMAN      STANDARD;      PRT;    10 AA.
AC   P34990;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Erythrocyte;
RA   Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA   Balant L., Hochstrasser D.F.;
RL   Submitted (FEB-1994) to Swiss-Prot.
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 4.77, its MW is: 26 kDa.
DR   SWISS-2DPAGE; P34990; HUMAN.
FT   NON_TER       10      10
SQ   SEQUENCE   10 AA;  1161 MW;  F72D82E9C44B1871 CRC64;
```

```
  Query Match             2.1%;  Score 23;  DB 1;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 1.9e+04;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        111 YGERFPD 117
              :|| | |
Db          3 HGENFXD 9


RESULT 42
CORZ_PERAM
ID   CORZ_PERAM     STANDARD;      PRT;    11 AA.
AC   P11496;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Corazonin.
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC   Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=89325572; PubMed=2753132;
RA   Veenstra J.A.;
RT   "Isolation and structure of corazonin, a cardioactive peptide from
RT   the American cockroach.";
RL   FEBS Lett. 250:231-234(1989).
CC   -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
CC       in the physiological regulation of the heart beat.
CC   -!- SUBCELLULAR LOCATION: Secreted.
DR   PIR; S05002; S05002.
KW   Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1387 MW;  C7CFF32D6415AB46 CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 11;
  Best Local Similarity   42.9%;  Pred. No. 2e+04;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        125 YGPGWVS 131
              |  || :
Db          5 YSRGWTN 11


RESULT 43
TKN4_PSEGU
ID   TKN4_PSEGU     STANDARD;      PRT;    11 AA.
AC   P42989;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Substance P-like peptide I (PG-SPI).
OS   Pseudophryne guentheri (Guenther's toadlet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC   Myobatrachinae; Pseudophryne.
OX   NCBI_TaxID=30349;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=90287814; PubMed=2356157;
RA   Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA   Roberts J.D., Melchiorri P., Erspamer V.;
RT   "Six novel tachykinin- and bombesin-related peptides from the skin of
RT   the Australian frog Pseudophryne guntheri.";
RL   Peptides 11:299-304(1990).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; E60409; E60409.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   InterPro; IPR008215; Tachykinin.
DR   Pfam; PF02202; Tachykinin; 1.
DR   SMART; SM00203; TK; 1.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1294 MW;  3A247C2CC9CB1AB7 CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 2e+04;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        116 PDENFKL 122
              ||| | |
Db          4 PDEFFGL 10


RESULT 44
ADFB_TENMO
ID   ADFB_TENMO     STANDARD;      PRT;    13 AA.
AC   P83109;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Antidiuretic factor B (ADFb).
OS   Tenebrio molitor (Yellow mealworm).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC   Tenebrionidae; Tenebrio.
OX   NCBI_TaxID=7067;
RN   [1]
RP   SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP   SYNTHESIS.
RC   TISSUE=Head;
RX   MEDLINE=22465067; PubMed=12576082;
RA   Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
RA   Hull J.J., Schooley D.A.;
RT   "Isolation, identification and localization of a second beetle
RT   antidiuretic peptide.";
RL   Peptides 24:27-34(2003).
CC   -!- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
CC       cGMP as second messenger. May function as an antidiuretic
CC       hormone.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
CC       pairs of bilaterally symmetrical cells in the protocerebrum.
CC   -!- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
KW   Neuropeptide; Hormone.
SQ   SEQUENCE   13 AA;  1562 MW;  0240A4504B8A632B CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 13;
  Best Local Similarity   50.0%;  Pred. No. 2.4e+04;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        103 DGTGGKSIYG 112
              ||:    |||
Db          3 DGSYKPHIYG 12


RESULT 45
MAST_VESCR
ID   MAST_VESCR     STANDARD;      PRT;    14 AA.
AC   P01516;
DT   21-JUL-1986 (Rel. 01, Created)
```

```
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Mastoparan C.
OS   Vespa crabro (European hornet).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC   Vespidae; Vespinae; Vespa.
OX   NCBI_TaxID=7445;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=84289390; PubMed=6206053;
RA   Argiolas A., Pisano J.J.;
RT   "Isolation and characterization of two new peptides, mastoparan C and
RT   crabrolin, from the venom of the European hornet, Vespa crabro.";
RL   J. Biol. Chem. 259:10106-10111(1984).
CC   -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC       that couple to phospholipase C.
DR   PIR; A01779; QMVHP2.
KW   Mast cell degranulation; Amidation.
FT   MOD_RES      14     14       AMIDATION.
SQ   SEQUENCE   14 AA;  1508 MW;  550C0ECA1D6AB1D7 CRC64;

  Query Match             2.1%;  Score 23;  DB 1;  Length 14;
  Best Local Similarity   62.5%;  Pred. No. 2.6e+04;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MKVLLAAA 8
              :| |||  |
Db          3 LKALLAVA 10


Search completed: August 30, 2004, 10:50:26
Job time : 36.8378 secs
```

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 62.5405 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	2.9	11	2	PT0218	T-cell receptor be
2	31	2.9	13	2	PH0796	T-cell receptor al
3	30	2.8	13	2	JQ1350	hypothetical prote
4	29	2.7	8	2	PT0279	Ig heavy chain CRD
5	29	2.7	8	2	PT0725	T-cell receptor be
6	29	2.7	8	2	PT0588	T-cell receptor be
7	29	2.7	12	2	G49410	t-complex polypept
8	28	2.6	8	2	A61348	red pigment-concen
9	28	2.6	10	2	A60421	hypertrehalosemic
10	28	2.6	10	2	S08997	hypertrehalosemic
11	28	2.6	10	2	S08998	hypertrehalosemic
12	28	2.6	10	2	A26381	hypertrehalosemic
13	28	2.6	11	2	S57575	T cell receptor V-
14	28	2.6	12	2	PH1458	T-cell receptor be
15	28	2.6	13	2	S78766	ribosomal protein
16	27.5	2.5	13	2	B56864	dipeptidyl-peptida
17	27	2.5	10	2	A46030	gonadoliberin I -
18	27	2.5	11	2	B60769	Ig H2 chain - Paci
19	27	2.5	14	2	PA0096	pyruvate decarboxy
20	27	2.5	14	2	PH0801	T-cell receptor al
21	26.5	2.4	12	2	S07206	kassinin - Senegal
22	26.5	2.4	13	2	A23695	myosin heavy chain
23	26.5	2.4	14	2	S33802	chaperone, TCP1-re
24	26.5	2.4	14	2	PH0747	T-cell receptor be
25	26	2.4	8	2	S55310	adipokinetic hormo
26	26	2.4	8	2	A58620	adipokinetic hormo
27	26	2.4	8	2	PT0554	T-cell receptor be
28	26	2.4	9	2	PT0231	Ig heavy chain CDR
29	26	2.4	10	1	RHAQ2	gonadoliberin II -
30	26	2.4	10	1	A61126	gonadoliberin - sp
31	26	2.4	10	2	B46030	gonadoliberin II -
32	26	2.4	10	2	A21114	gonadoliberin - ch
33	26	2.4	11	2	C38887	T-cell receptor ga
34	26	2.4	12	2	S26544	T-cell receptor be
35	26	2.4	12	2	S65730	hemoglobin, extrac
36	26	2.4	13	2	C53275	Ig kappa-1 chain J
37	26	2.4	14	2	JN0390	histamine-releasin
38	26	2.4	14	2	PH0795	T-cell receptor al
39	25	2.3	8	2	S15422	adipokinetic hormo
40	25	2.3	8	2	A33995	adipokinetic hormo
41	25	2.3	8	2	A58641	adipokinetic hormo
42	25	2.3	8	2	S21663	neuropeptide - flo
43	25	2.3	8	2	PT0595	T-cell receptor be
44	25	2.3	10	2	B33995	hypotrehalosemic h
45	25	2.3	10	2	A60476	S-layer protein -

ALIGNMENTS

RESULT 1
PT0218
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0218
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0218
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 2.9%; Score 31; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy        102 GDGTGGKSIY 111
              | | || ::|
Db          2 GAGQGGNTLY 11
```

RESULT 2
PH0796
T-cell receptor alpha chain (F15) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0796
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-re
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0796
A;Molecule type: mRNA
A;Residues: 1-13 <CAS>
A;Cross-references: EMBL:X60901
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 2.9%; Score 31; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 9.6e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy        102 GDGTGGKSIYG 112
              | |  || |:|
Db          3 GTGNTGKLIFG 13
```

RESULT 3

JQ1350
hypothetical protein, 1.3K (rps16 5' region) - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C;Accession: JQ1350
R;Bradshaw, R.E.; Pillar, T.M.
Gene 108, 157-162, 1991
A;Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gene fr
A;Reference number: JQ1349; MUID:92104500; PMID:1761226
A;Accession: JQ1350
A;Molecule type: DNA
A;Residues: 1-13 <BRA>
A;Cross-references: GB:M65259; NID:g168087; PID:g168089
A;Experimental source: strain R153

Query Match 2.8%; Score 30; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy         67 NFVALATGEK 76
              | |  |||:|
Db          2 NMVCAATGKK 11
```

RESULT 4
PT0279
Ig heavy chain CRD3 region (clone 4-91A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0279
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0279
A;Molecule type: DNA
A;Residues: 1-8 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 2.7%; Score 29; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        102 GDGTGG 107
              ||| ||
Db          3 GDGRGG 8
```

RESULT 5
PT0725
T-cell receptor beta chain V-D-J region (140-2I) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0725
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0725
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-8 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 2.7%; Score 29; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        102 GDGTGG 107
              ||| ||
Db          3 GDGLGG 8
```

RESULT 6
PT0588
T-cell receptor beta chain V-D-J region (141-1CB) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0588
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0588
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 2.7%; Score 29; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        102 GDGTGG 107
              || |||
Db          3 GDATGG 8
```

RESULT 7
G49410
t-complex polypeptide 1 homolog (peak 6b fraction) - rabbit (fragment)
N;Alternate names: chaperonin homolog (peak 6b)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 04-Sep-1998
C;Accession: G49410
R;Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Am
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A;Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela
A;Reference number: A49410; MUID:94089752; PMID:7903455
A;Accession: G49410
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <ROM>
A;Experimental source: reticulocyte
C;Superfamily: molecular chaperone t-complex-type

Query Match 2.7%; Score 29; DB 2; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy        130 VSMANAGKDTN 140
              : :|| | ||:
Db          1 ILIANTGMDTD 11
```

RESULT 8
A61348
red pigment-concentrating hormone - northern shrimp
N;Alternate names: blanching hormone
C;Species: Pandalus borealis (northern shrimp)
C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61348; S07139
R;Fernlund, P.; Josefsson, L.
Science 177, 173-175, 1972
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
A;Reference number: A61348; MUID:72228738; PMID:5041363
A;Accession: A61348
A;Molecule type: protein
A;Residues: 1-8 <FER1>
R;Fernlund, P.
Biochim. Biophys. Acta 371, 304-311, 1974
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore
A;Reference number: S07139; MUID:75054965; PMID:4433569

A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E',2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFSPGW 8

RESULT 9
A60421
hypertrehalosemic hormone - German cockroach
N;Alternate names: Bld-HrTH
C;Species: Blattella germanica (German cockroach)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C;Accession: A60421; S09137
R;Veenstra, J.A.; Camps, F.
Neuropeptides 15, 107-109, 1990
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blatte
A;Reference number: A60421; MUID:91179584; PMID:2080017
A;Accession: A60421
A;Molecule type: protein
A;Residues: 1-10 <VEE>
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFSPGW 8

RESULT 10
S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08997
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFSPGW 8

RESULT 11
S08998
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08998
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardm
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFSPGW 8

RESULT 12
A26381
hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: A26381
R;Gade, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpus cardiac
A;Reference number: A26381; MUID:87100208; PMID:3801028
A;Accession: A26381
A;Molecule type: protein
A;Residues: 1-10 <GAD>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFSPGW 8

RESULT 13
S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A;Reference number: S57494
A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor

Query Match 2.6%; Score 28; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 106 GGKSIYG 112
||| |:|
Db 5 GGKLIFG 11

RESULT 14
PH1458
T-cell receptor beta chain (clone 332/1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
C;Accession: PH1458; S26543
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1458
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Experimental source: cytolytic T-lymphocyte, clone 332/1K
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CA2>
A;Cross-references: EMBL:X67993
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/C44
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell

Query Match 2.6%; Score 28; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 95 QGGDFTRG 102
|| |:| |
Db 5 QGSDYTFG 12

RESULT 15
S78766
ribosomal protein MRP-S28, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78766
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78766
A;Molecule type: protein
A;Residues: 1-13 <GRA>
C;Keywords: mitochondrion
F;1-13/Product: ribosomal protein MRP-S28 (fragment) #status experimental <MAT>

Query Match 2.6%; Score 28; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 62 PKTVDNFVAL 71
|| |::| ::
Db 3 PKNVESFASM 12

RESULT 16
B56864
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: B56864
R;Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993
A;Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border mem
A;Reference number: A56864; MUID:93136203; PMID:8093665
A;Accession: B56864
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <PLA>
A;Experimental source: renal brush-border membrane vesicles
C;Keywords: dipeptidylpeptide hydrolase

Query Match 2.5%; Score 27.5; DB 2; Length 13;
Best Local Similarity 35.0%; Pred. No. 1.9e+04;
Matches 7; Conservative 2; Mismatches 2; Indels 9; Gaps 1;

Qy 149 VKTAWLDGKHVVFGKVLEGM 168
:|| | ||| |:
Db 1 MKTPW---------KVLSGL 11

RESULT 17
A46030
gonadoliberin I - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Dec-1998
C;Accession: A46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: A46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 2.5%; Score 27; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.6e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 123 KHYGPGWV 130
:|: ||:
Db 1 QHWSHGWL 8

RESULT 18
B60769
Ig H2 chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C;Accession: B60769
R;Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A;Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A;Reference number: A60769; MUID:91060965; PMID:2123225
A;Accession: B60769
A;Status: preliminary
A;Molecule type: protein

A;Residues: 1-11 <HAN>

Query Match 2.5%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy         90 KDFMIQ 95
              :|||||
Db          4 EDFMIQ 9
```

RESULT 19
PA0096
pyruvate decarboxylase (EC 4.1.1.1) 1 - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0096
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotrich
A;Reference number: PA0051
A;Accession: PA0096
A;Molecule type: protein
A;Residues: 1-14 <CHO>
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 2.5%; Score 27; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy         36 VKVYFDLRIGDE 47
              |  |||   ||:
Db          1 VXAYFDGLPGDQ 12
```

RESULT 20
PH0801
T-cell receptor alpha chain (J5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0801
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0801
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60909
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 2.5%; Score 27; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.2e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy        104 GTGGKSIYG 112
              |||  |  :|
Db          6 GTGSKLSFG 14
```

RESULT 21
S07206
kassinin - Senegal running frog
C;Species: Kassina senegalensis (Senegal running frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000
C;Accession: S07206
R;Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.
Experientia 33, 857-858, 1977
A;Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide fro
A;Reference number: S07206; MUID:77246385; PMID:891753
A;Accession: S07206
A;Molecule type: protein
A;Residues: 1-12 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 2.4%; Score 26.5; DB 2; Length 12;
Best Local Similarity 63.6%; Pred. No. 2.1e+04;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

```
Qy         61 VPKTVDNFVAL 71
              |||: | ||  |
Db          2 VPKS-DQFVGL 11
```

RESULT 22
A23695
myosin heavy chain, smooth muscle - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 02-Feb-2001
C;Accession: A23695
R;Garabedian, T.E.; Yount, R.G.
J. Biol. Chem. 265, 22547-22553, 1990
A;Title: Direct photoaffinity labeling of gizzard myosin with [3H]uridine diphosphate pla
A;Reference number: A23695; MUID:91093106; PMID:1979981
A;Accession: A23695
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <GAR>
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop; smooth muscle
F;2-9/Region: nucleotide-binding motif A (P-loop)

Query Match 2.4%; Score 26.5; DB 2; Length 13;
Best Local Similarity 53.8%; Pred. No. 2.3e+04;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

```
Qy         73 TGEKGFG-YKNSK 84
              ||| | |  :|:|
Db          1 TGESGAGKTENTK 13
```

RESULT 23
S33802
chaperone, TCP1-related - oat
C;Species: Avena sativa (oat)
C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C;Accession: S33802
R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefe
Nature 363, 644-648, 1993
A;Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo
A;Reference number: S33800; MUID:93288140; PMID:8099715
A;Accession: S33802
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <MUM>

Query Match 2.4%; Score 26.5; DB 2; Length 14;
Best Local Similarity 46.2%; Pred. No. 2.5e+04;
Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

```
Qy        118 ENFKLKHYGPGWV 130
              |: ||   || |:
Db          3 ESAKL---GPWWI 12
```

RESULT 24
PH0747
T-cell receptor beta chain (M1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0747
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0747
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60838
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.5e+04;
Matches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

Qy 104 GTGGKSIYGERF 115
|||| : |:|
Db 4 GTGG---FAEQF 12

RESULT 25
S55310
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N;Alternate names: Psi-AKH
C;Species: Pseudagrion inconspicuum
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: S55310
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: S55310
A;Molecule type: protein
A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFTPGW 8

RESULT 26
A58620
adipokinetic hormone - damselfly (Ischnura senegalensis)
C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: A58620
A;Molecule type: protein
A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
:: |||
Db 3 NFTPGW 8

RESULT 27
PT0554
T-cell receptor beta chain V-D-J region (126-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0554
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0554
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 72 ATGEKGFG 79
|:|::| |
Db 1 ASGDEGLG 8

RESULT 28
PT0231
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0231
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0231
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 2.4%; Score 26; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 125 YGPGWVS 131
: ||||
Db 3 HSSGWVS 9

RESULT 29
RHAQ2
gonadoliberin II - American alligator
N;Alternate names: gonadotropin-releasing hormone II
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: B60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
A;Reference number: A60066; MUID:91352338; PMID:1882082
A;Accession: B60066
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 2.4%; Score 26; DB 1; Length 10;

Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy        123 KHYGPGW 129
              :|:  ||
Db          1 QHWSHGW 7
```

RESULT 30
A61126
gonadoliberin - spotted ratfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Hydrolagus colliei (spotted ratfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 18-Mar-1997
C;Accession: A61126
R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
Gen. Comp. Endocrinol. 82, 152-161, 1991
A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocep
A;Reference number: A61126; MUID:91340067; PMID:1678723
A;Accession: A61126
A;Molecule type: protein
A;Residues: 1-10 <LOV>
A;Experimental source: brain
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 2.4%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy        123 KHYGPGW 129
              :|:  ||
Db          1 QHWSHGW 7
```

RESULT 31
B46030
gonadoliberin II - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jan-2003
C;Accession: B46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: B46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy        123 KHYGPGW 129
              :|:  ||
Db          1 QHWSHGW 7
```

RESULT 32
A21114
gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A;Title: Characterization of a teleost gonadotropin-releasing hormone.
A;Reference number: A21114; MUID:83195140; PMID:6341999
A;Accession: A21114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>

Query Match 2.4%; Score 26; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy        123 KHYGPGWV 130
              :|:  ||:
Db          1 QHWSYGWL 8
```

RESULT 33
C38887
T-cell receptor gamma chain (5a.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+04;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy        135 AGKDTNG 141
              ||:|::|
Db          4 AGRDSSG 10
```

RESULT 34
S26544
T-cell receptor beta chain (clone Cw3/HLA1C8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26544
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widn
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptors
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26544
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67994
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1C8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy         95 QGGDFTRG 102
              || |:| |
Db          5 QGTDYTFG 12
```

RESULT 35
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

```
C;Accession: S65730
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65730
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FUS>

  Query Match              2.4%;  Score 26;  DB 2;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         21 GPSAAD 26
              |||| |
Db          2 GPSARD 7


RESULT 36
C53275
Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C;Accession: C53275
R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A;Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A;Reference number: A53275; MUID:91372868; PMID:1909995
A;Accession: C53275
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <AYA>
A;Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56164)
C;Comment: This J3 segment may not be functional because of substitutions in the 7 mer a
C;Keywords: heterotetramer; immunoglobulin

  Query Match              2.4%;  Score 26;  DB 2;  Length 13;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+04;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         100 TRGDGT 105
               ||| ||
Db           2 TRGPGT 7


RESULT 37
JN0390
histamine-releasing peptide II - oriental hornet
N;Alternate names: venom protein HR-2
C;Species: Vespa orientalis (oriental hornet)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C;Accession: JN0390; S10919
R;Miroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus
Bioorg. Khim. 7, 1467-1477, 1981
A;Title: Structure and properties of histamine releasing peptides from the venom of Vesp
A;Reference number: JN0389
A;Accession: JN0390
A;Molecule type: protein
A;Residues: 1-14 <MIR>
R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St
A;Reference number: S06445
A;Accession: S10919
A;Molecule type: protein
A;Residues: 1-14 <TUI>
C;Superfamily: crabrolin
C;Keywords: amidated carboxyl end; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

  Query Match              2.4%;  Score 26;  DB 2;  Length 14;
  Best Local Similarity   30.0%;  Pred. No. 2.7e+04;
  Matches    3;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         159 VVFGKVLEGM 168
               :: ||:::|:
Db           4 LILGKLVKGL 13


RESULT 38
PH0795
T-cell receptor alpha chain (K1 V-alpha-4.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0795
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0795
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60900
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

  Query Match              2.4%;  Score 26;  DB 2;  Length 14;
  Best Local Similarity   36.4%;  Pred. No. 2.7e+04;
  Matches    4;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         102 GDGTGGKSIYG 112
               |:|:  |  :|
Db           4 GEGSNAKLTFG 14


RESULT 39
S15422
adipokinetic hormone - cockchafer
C;Species: Melolontha melolontha (cockchafer)
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: S15422
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: S15422
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

  Query Match              2.3%;  Score 25;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         124 HYGPGW 129
               :| | |
Db           3 NYSPDW 8


RESULT 40
A33995
adipokinetic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: A33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: A33995
A;Molecule type: protein
```

A;Residues: 1-8 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy        125 YGPGW 129
              : |||
Db          4 FTPGW 8
```

RESULT 41
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: A58641
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy        124 HYGPGW 129
              :| | |
Db          3 NYSPDW 8
```

RESULT 42
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of varic
ectrometry.
A;Reference number: S21663; MUID:92265187; PMID:1586453
A;Accession: S21663
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy        124 HYGPGW 129
              :| | |
Db          3 NYSPDW 8
```

RESULT 43
PT0595
T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0595
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0595
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy        103 DGTGG 107
              :||||
Db          4 EGTGG 8
```

RESULT 44
B33995
hypotrehalosemic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: B33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalc
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 2.3%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy        125 YGPGW 129
              : |||
Db          4 FTPGW 8
```

RESULT 45
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C;Accession: A60476
R;Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A;Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A;Reference number: A60476; MUID:90078111; PMID:2592346
A;Accession: A60476
A;Molecule type: protein
A;Residues: 1-10 <LUC>
C;Comment: The S-layer, or surface array, is the outermost component of several archaebac

Query Match 2.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy        112 GERFPD 117
              |: |||
Db          2 GKTFPD 7
```

Search completed: August 30, 2004, 10:58:53
Job time : 62.5405 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 254.378 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	7.7	14	15	US-10-394-980-52	Sequence 52, Appl
2	54	5.0	14	12	US-10-014-340-347	Sequence 347, App
3	50	4.6	9	16	US-10-447-161-85	Sequence 85, Appl
4	50	4.6	9	16	US-10-788-016-2	Sequence 2, Appli
5	49	4.5	9	16	US-10-447-161-84	Sequence 84, Appl
6	49	4.5	9	16	US-10-788-016-1	Sequence 1, Appli
7	47	4.3	9	16	US-10-788-016-9	Sequence 9, Appli
8	36	3.3	11	10	US-09-972-656-7	Sequence 7, Appli
9	36	3.3	13	9	US-09-873-637-9	Sequence 9, Appli
10	36	3.3	13	10	US-09-876-904A-242	Sequence 242, App
11	36	3.3	13	13	US-10-038-612-168	Sequence 168, App
12	35	3.2	9	16	US-10-264-309-118	Sequence 118, App
13	35	3.2	11	16	US-10-356-257-142	Sequence 142, App
14	35	3.2	13	14	US-10-300-694A-66	Sequence 66, Appl
15	35	3.2	14	12	US-10-247-839-101	Sequence 101, App
16	34	3.1	9	12	US-09-988-493-293	Sequence 293, App
17	34	3.1	9	12	US-10-014-340-209	Sequence 209, App
18	34	3.1	11	12	US-09-995-388-8	Sequence 8, Appli
19	34	3.1	12	12	US-09-995-388-5	Sequence 5, Appli
20	34	3.1	12	14	US-10-193-477-146	Sequence 146, App
21	34	3.1	12	14	US-10-193-477-168	Sequence 168, App
22	32.5	3.0	13	14	US-10-017-193-8	Sequence 8, Appli
23	32	3.0	9	9	US-09-802-077-50	Sequence 50, Appl
24	32	3.0	9	9	US-09-802-096-50	Sequence 50, Appl
25	32	3.0	9	10	US-09-925-179-50	Sequence 50, Appl
26	32	3.0	9	14	US-10-223-172A-27	Sequence 27, Appl
27	32	3.0	9	14	US-10-224-999A-27	Sequence 27, Appl
28	32	3.0	10	9	US-09-802-077-17	Sequence 17, Appl
29	32	3.0	10	9	US-09-802-077-46	Sequence 46, Appl
30	32	3.0	10	9	US-09-802-096-17	Sequence 17, Appl
31	32	3.0	10	9	US-09-802-096-46	Sequence 46, Appl
32	32	3.0	10	10	US-09-925-179-17	Sequence 17, Appl
33	32	3.0	10	10	US-09-925-179-46	Sequence 46, Appl
34	32	3.0	10	10	US-09-755-630A-33	Sequence 33, Appl
35	32	3.0	10	14	US-10-223-172A-33	Sequence 33, Appl
36	32	3.0	10	14	US-10-224-999A-33	Sequence 33, Appl
37	32	3.0	11	12	US-09-995-388-9	Sequence 9, Appli
38	32	3.0	12	12	US-10-601-837-103	Sequence 103, App
39	32	3.0	12	14	US-10-224-999A-2922	Sequence 2922, Ap
40	32	3.0	13	10	US-09-991-225-19	Sequence 19, Appl
41	32	3.0	13	10	US-09-991-225-38	Sequence 38, Appl
42	32	3.0	13	12	US-10-369-405-19	Sequence 19, Appl
43	32	3.0	13	12	US-10-369-405-38	Sequence 38, Appl
44	32	3.0	13	14	US-10-224-999A-2931	Sequence 2931, Ap
45	32	3.0	13	14	US-10-224-999A-2932	Sequence 2932, Ap

ALIGNMENTS

RESULT 1
US-10-394-980-52
; Sequence 52, Application US/10394980
; Publication No. US20040005633A1
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: part of CYPB_HUMAN (peptidyl-prolyl cis-trans isomerase B)
US-10-394-980-52

Query Match 7.7%; Score 83; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 HYGPGWVSMANAGK 137
||||||||||||||
Db 1 HYGPGWVSMANAGK 14

RESULT 2
US-10-014-340-347
; Sequence 347, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-347

Query Match 5.0%; Score 54; DB 12; Length 14;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy         88 VIKDFMIQGGDFTR 101
              :|  || |||||||
Db          1 IIPGFMCQGGDFTR 14
```

RESULT 3
US-10-447-161-85
; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match 4.6%; Score 50; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         91 DFMIQGGDF 99
              |||||||||
Db          1 DFMIQGGDF 9
```

RESULT 4
US-10-788-016-2
; Sequence 2, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
; OTHER INFORMATION: to the 99th residue of cyclophillin B
US-10-788-016-2

Query Match 4.6%; Score 50; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         91 DFMIQGGDF 99
              |||||||||
Db          1 DFMIQGGDF 9
```

RESULT 5
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 4.5%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         84 KFHRVIKDF 92
              |||||||||
Db          1 KFHRVIKDF 9
```

RESULT 6
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial

; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophillin B
US-10-788-016-1

Query Match 4.5%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          84 KFHRVIKDF 92
               |||||||||
Db           1 KFHRVIKDF 9
```

RESULT 7
US-10-788-016-9
; Sequence 9, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
; OTHER INFORMATION: residues from the 91st residue to the 99th residue of
; OTHER INFORMATION: cyclophillin B
US-10-788-016-9

Query Match 4.3%; Score 47; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          91 DFMIQGGDF 99
               |:|||||||
Db           1 DYMIQGGDF 9
```

RESULT 8
US-09-972-656-7
; Sequence 7, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-7

Query Match 3.3%; Score 36; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.3e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy         102 GDGTGGKSIY 111
               ||  ||||::
Db           2 GDNLGGKSLH 11
```

RESULT 9
US-09-873-637-9
; Sequence 9, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for SEQ ID NOs:3-8.
US-09-873-637-9

Query Match 3.3%; Score 36; DB 9; Length 13;
Best Local Similarity 63.6%; Pred. No. 4.2e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          97 GDFTRGDGTGG 107
               | | || | ||
Db           3 GGFGRGGGRGG 13
```

RESULT 10
US-09-876-904A-242
; Sequence 242, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 242
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: XPC gene product
US-09-876-904A-242

Query Match 3.3%; Score 36; DB 10; Length 13;
Best Local Similarity 58.8%; Pred. No. 4.2e+03;
Matches 10; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

```
Qy          21 GPSAADEKKKGPKVTVK 37
               ||:    |||  |||||
Db           1 GPA----KKKVAKVTVK 13
```

RESULT 11
US-10-038-612-168
; Sequence 168, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:

```
;  APPLICANT: Ben-Sasson, Shmuel A.
;  TITLE OF INVENTION: Short Peptides Which Selectively
;  TITLE OF INVENTION:  Modulate the Activity of Protein Kinases
;  FILE REFERENCE: 1242.1029-000 (CMCC-679)
;  CURRENT APPLICATION NUMBER: US/10/038,612
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US 09/161,094
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MYRISTATE
;   LOCATION: (1)...(0)
;   NAME/KEY: AMIDATION
;   LOCATION: (0)...(13)
;   OTHER INFORMATION: TrkB
US-10-038-612-168

  Query Match             3.3%;  Score 36;  DB 13;  Length 13;
  Best Local Similarity   66.7%;  Pred. No. 4.2e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        119 NFKLKHYGP 127
              |||| : :||
Db          3 NFKLRAHGP 11


RESULT 12
US-10-264-309-118
; Sequence 118, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
;  APPLICANT: DURHAM, L. KATHRYN
;  APPLICANT:  FRIEDMAN, DAVID L.
;  APPLICANT:  HERATH, HERATH
;  APPLICANT:  KIMMEL, LIDA H.
;  APPLICANT:  PAREKH, RAJESH B.
;  APPLICANT:  POTTER, DAVID M.
;  APPLICANT:  ROHLFF, CHRISTIAN
;  APPLICANT:  SILBER, B. MICHAEL
;  APPLICANT:  SNYDER, PETER J.
;  APPLICANT:  SOARES, HOLLY D.
;  APPLICANT:  STIGER, THOMAS R.
;  APPLICANT:  SUNDERLAND, P. TREY
;  APPLICANT:  TOWNSEND, ROBERT R.
;  APPLICANT:  WHITE, W. FROST
;  APPLICANT:  WILLIAMS, STEPHEN A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
;  TITLE OF INVENTION:  INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
;  FILE REFERENCE: POA-002.01
;  CURRENT APPLICATION NUMBER: US/10/264,309
;  CURRENT FILING DATE:  2002-10-03
;  PRIOR APPLICATION NUMBER: 60/326,708
;  PRIOR FILING DATE: 2001-10-03
;  NUMBER OF SEQ ID NOS: 491
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 118
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-309-118

  Query Match             3.2%;  Score 35;  DB 16;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        115 FPDENFKLK 123
              | |||| ||
Db          1 FEDENFLLK 9


RESULT 13
US-10-356-257-142
; Sequence 142, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
;  APPLICANT: LAZARUS, ROBERT A.
;  APPLICANT:  MAUN, HENRY R.
;  TITLE OF INVENTION: FVIIa Antagonists
;  FILE REFERENCE: P1950R1
;  CURRENT APPLICATION NUMBER: US/10/356,257
;  CURRENT FILING DATE:  2003-01-30
;  PRIOR APPLICATION NUMBER: US 60/355,420
;  PRIOR FILING DATE: 2002-02-06
;  NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 142
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is synthesized
US-10-356-257-142

  Query Match             3.2%;  Score 35;  DB 16;  Length 11;
  Best Local Similarity   77.8%;  Pred. No. 4.3e+03;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         96 GGDFTRGDG 104
              ||| ||| |
Db          2 GGDSTRGYG 10


RESULT 14
US-10-300-694A-66
; Sequence 66, Application US/10300694A
; Publication No. US20030185870A1
; GENERAL INFORMATION:
;  APPLICANT: Duke University
;  APPLICANT:  Grinstaff, Mark W.
;  APPLICANT:  Kenan, Daniel J.
;  APPLICANT:  Walsh, Elisabeth B.
;  APPLICANT:  Middleton, Crystan
;  TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
;  FILE REFERENCE: 180/143/2
;  CURRENT APPLICATION NUMBER: US/10/300,694A
;  CURRENT FILING DATE:  2003-05-07
;  PRIOR APPLICATION NUMBER: US 60/331,843
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Polycarbonate-binding peptide 66
US-10-300-694A-66

  Query Match             3.2%;  Score 35;  DB 14;  Length 13;
  Best Local Similarity   41.7%;  Pred. No. 5.4e+03;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        125 YGPGWVSMANAG 136
              :| ||::  | |
Db          1 FGHGWLNTLNLG 12


RESULT 15
US-10-247-839-101
; Sequence 101, Application US/10247839
; Publication No. US20040058400A1
;   GENERAL INFORMATION:
```

; APPLICANT: Holliger, Kaspar-Philipp
; Griffiths, Andrew D
; Hoogenboom, Hendricus RJM
; Malmqvist, Magnus
; Marks, James D
; McGuinness, Brian T
; Pope, Anthony R
; Prospero, Terence D
; Winter, Gregory P
; TITLE OF INVENTION: Multivalent and Multispecific Binding
; Proteins, Their Manufacture and Use
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun
; STREET: 6300 Sears Tower 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/247,839
; FILING DATE: 20-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,979
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/448,418
; FILING DATE: 14-MAY-1996
; APPLICATION NUMBER: PCT/GB93/02492
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: GB 9225453.1
; FILING DATE: 04-DEC-1992
; APPLICATION NUMBER: GB 9300816.7
; FILING DATE: 16-JAN-1993
; APPLICATION NUMBER: EP 93303614.7
; FILING DATE: 10-MAY-1993
; APPLICATION NUMBER: GB 9319969.3
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32651
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide linker
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-247-839-101

Query Match 3.2%; Score 35; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 6e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```
Qy          96 GGDFTRGDGTGGKS 109
               ||  : | |:|| |
Db           1 GGGGSGGGGSGGSS 14
```

RESULT 16
US-09-988-493-293
; Sequence 293, Application US/09988493
; Publication No. US20030064419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-293

Query Match 3.1%; Score 34; DB 12; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         115 FPDENFKLK 123
               | |||| ||
Db           1 FEDENFILK 9
```

RESULT 17
US-10-014-340-209
; Sequence 209, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 209
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-209

Query Match 3.1%; Score 34; DB 12; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         115 FPDENFKLK 123
               | |||| ||
Db           1 FEDENFILK 9
```

RESULT 18
US-09-995-388-8
; Sequence 8, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
; APPLICANT: Carpenter, Jr., Alan P.
; TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
; TITLE OF INVENTION: RECEPTOR TARGETED IMAGING AGENT
; FILE REFERENCE: BMS-2201
; CURRENT APPLICATION NUMBER: US/09/995,388
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/253,324
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2

```
; SEQ ID NO 8
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-995-388-8

  Query Match             3.1%;  Score 34;  DB 12;  Length 11;
  Best Local Similarity   85.7%;  Pred. No. 5.5e+03;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              ||| |||
Db          4 GDFKRGD 10


RESULT 19
US-09-995-388-5
; Sequence 5, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
;  APPLICANT: Carpenter, Jr., Alan P.
;  TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
;  TITLE OF INVENTION:  RECEPTOR TARGETED IMAGING AGENT
;  FILE REFERENCE: BMS-2201
;  CURRENT APPLICATION NUMBER: US/09/995,388
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: US 60/253,324
;  PRIOR FILING DATE: 2000-11-27
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-995-388-5

  Query Match             3.1%;  Score 34;  DB 12;  Length 12;
  Best Local Similarity   85.7%;  Pred. No. 6.2e+03;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              ||| |||
Db          5 GDFKRGD 11


RESULT 20
US-10-193-477-146
; Sequence 146, Application US/10193477
; Publication No. US20030195163A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
;  TITLE OF INVENTION:  LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0153 NP
;  CURRENT APPLICATION NUMBER: US/10/193,477
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: US 60/304,888
;  PRIOR FILING DATE: 2001-07-11
;  PRIOR APPLICATION NUMBER: US 60/372,147
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-193-477-146

  Query Match             3.1%;  Score 34;  DB 14;  Length 12;
  Best Local Similarity   70.0%;  Pred. No. 6.2e+03;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 VFFLLLPGPS 23
              :| |||||  |
Db          3 LFLLLLPGGS 12


RESULT 21
US-10-193-477-168
; Sequence 168, Application US/10193477
; Publication No. US20030195163A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
;  TITLE OF INVENTION:  LEUCINE RICH REPEATS AND IMMUNOLOGOBULIN FOLDS, BGS2, 3, AND 4,
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0153 NP
;  CURRENT APPLICATION NUMBER: US/10/193,477
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: US 60/304,888
;  PRIOR FILING DATE: 2001-07-11
;  PRIOR APPLICATION NUMBER: US 60/372,147
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-193-477-168

  Query Match             3.1%;  Score 34;  DB 14;  Length 12;
  Best Local Similarity   70.0%;  Pred. No. 6.2e+03;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         14 VFFLLLPGPS 23
              :| |||||  |
Db          3 LFLLLLPGGS 12


RESULT 22
US-10-017-193-8
; Sequence 8, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
;  APPLICANT: Dang, Mai Huong
;  APPLICANT:  Chiu, Phillip
;  TITLE OF INVENTION: Surface Coating Method and Coated Device
;  FILE REFERENCE: 52200-8010
;  CURRENT APPLICATION NUMBER: US/10/017,193
;  CURRENT FILING DATE:  2001-12-12
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: attachment peptide from collagen
US-10-017-193-8

  Query Match             3.0%;  Score 32.5;  DB 14;  Length 13;
  Best Local Similarity   70.0%;  Pred. No. 1e+04;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         39 YFDLRI-GDE 47
              |||||: ||:
Db          4 YFDLRLKGDK 13


RESULT 23
```

US-09-802-077-50
; Sequence 50, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-077-50

Query Match 3.0%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8
```

RESULT 24
US-09-802-096-50
; Sequence 50, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-096-50

Query Match 3.0%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8
```

RESULT 25
US-09-925-179-50
; Sequence 50, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-925-179-50

Query Match 3.0%; Score 32; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8
```

RESULT 26
US-10-223-172A-27
; Sequence 27, Application US/10223172A
; Publication No. US20030138444A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Zavitz, Kenton
; APPLICANT: Wettstein, Daniel Albert
; APPLICANT: Morham, Scott
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
; FILE REFERENCE: 5003.01
; CURRENT APPLICATION NUMBER: US/10/223,172A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/313,239
; PRIOR FILING DATE: 2001-08-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-223-172A-27

Query Match 3.0%; Score 32; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          20 PGPSAADEK 28
               |||||  |:
Db           1 PGPSAPPEE 9
```

RESULT 27
US-10-224-999A-27
; Sequence 27, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified HIV Peptide
US-10-224-999A-27

Query Match 3.0%; Score 32; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          20 PGPSAADEK 28
               |||||  |:
Db           1 PGPSAPPEE 9
```

RESULT 28
US-09-802-077-17
; Sequence 17, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-17

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         153 WLDGK 157
               |||||
Db           5 WLDGK 9
```

RESULT 29
US-09-802-077-46
; Sequence 46, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-077-46

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         153 WLDGK 157
               |||||
Db           5 WLDGK 9
```

RESULT 30
US-09-802-096-17
; Sequence 17, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-17

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 31
US-09-802-096-46
; Sequence 46, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION:  Method of Preventing the Onset of Allergic Disorders (as amended
;  FILE REFERENCE:  P0718P2C3US
;  CURRENT APPLICATION NUMBER: US/09/802,096
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  US 08/405,617
;  PRIOR FILING DATE:  1995-03-15
;  PRIOR APPLICATION NUMBER:  US 08/185,899
;  PRIOR FILING DATE:  1994-01-26
;  PRIOR APPLICATION NUMBER:  PCT/US92/06860
;  PRIOR FILING DATE:  1992-08-14
;  PRIOR APPLICATION NUMBER:  US 07/879,495
;  PRIOR FILING DATE:  1992-05-07
;  PRIOR APPLICATION NUMBER:  US 07/744,768
;  PRIOR FILING DATE:  1991-08-14
;  NUMBER OF SEQ ID NOS:  64
; SEQ ID NO 46
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-096-46

  Query Match             3.0%;  Score 32;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 32
US-09-925-179-17
; Sequence 17, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P0718P2C1D1C1US
;  CURRENT APPLICATION NUMBER: US/09/925,179
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 08/466,163
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: PCT/US92/06860
;  PRIOR FILING DATE: 1992-08-14
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-179-17

  Query Match             3.0%;  Score 32;  DB 10;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 33
US-09-925-179-46
; Sequence 46, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
;  FILE REFERENCE: P0718P2C1D1C1US
;  CURRENT APPLICATION NUMBER: US/09/925,179
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 08/466,163
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: PCT/US92/06860
;  PRIOR FILING DATE: 1992-08-14
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 46
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-925-179-46

  Query Match             3.0%;  Score 32;  DB 10;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 34
US-09-755-630A-33
; Sequence 33, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;  CURRENT APPLICATION NUMBER: US/09/755,630A
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 293
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-33

  Query Match              3.0%;  Score 32;  DB 10;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 8e+03;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        201 KPFAIAKE 208
              :||| |||
Db          3 RPFAAAKE 10


RESULT 35
US-10-223-172A-33
; Sequence 33, Application US/10223172A
; Publication No. US20030138444A1
; GENERAL INFORMATION:
;  APPLICANT: Myriad Genetics, Inc.
;  APPLICANT:  Zavitz, Kenton
;  APPLICANT:  Wettstein, Daniel Albert
;  APPLICANT:  Morham, Scott
;  APPLICANT:  Hobden, Adrian
;  TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
;  FILE REFERENCE: 5003.01
;  CURRENT APPLICATION NUMBER: US/10/223,172A
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/313,239
;  PRIOR FILING DATE: 2001-08-18
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
US-10-223-172A-33

  Query Match              3.0%;  Score 32;  DB 14;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 8e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         20 PGPSAADEK 28
              |||||  |:
Db          2 PGPSAPPEE 10


RESULT 36
US-10-224-999A-33
; Sequence 33, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
;  APPLICANT: Myriad Genetics, Inc.
;  APPLICANT:  Morham, Scott
;  APPLICANT:  Zavitz, Kenton
;  APPLICANT:  Hobden, Adrian
;  TITLE OF INVENTION: Composition and Method for Treating Viral Infection
;  FILE REFERENCE: 5004.01
;  CURRENT APPLICATION NUMBER: US/10/224,999A
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/313,695
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 3484
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Modified HIV Peptide
US-10-224-999A-33

  Query Match              3.0%;  Score 32;  DB 14;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 8e+03;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         20 PGPSAADEK 28
              |||||  |:
Db          2 PGPSAPPEE 10


RESULT 37
US-09-995-388-9
; Sequence 9, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
;  APPLICANT: Carpenter, Jr., Alan P.
;  TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
;  TITLE OF INVENTION:  RECEPTOR TARGETED IMAGING AGENT
;  FILE REFERENCE: BMS-2201
;  CURRENT APPLICATION NUMBER: US/09/995,388
;  CURRENT FILING DATE:  2001-11-27
;  PRIOR APPLICATION NUMBER: US 60/253,324
;  PRIOR FILING DATE: 2000-11-27
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-995-388-9

  Query Match              3.0%;  Score 32;  DB 12;  Length 11;
  Best Local Similarity   71.4%;  Pred. No. 9.1e+03;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         97 GDFTRGD 103
              ||: |||
Db          5 GDYVRGD 11


RESULT 38
US-10-601-837-103
; Sequence 103, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
;  APPLICANT: Holt, Gordon D
;  APPLICANT:  Kelly, Michael D
;  APPLICANT:  Kennedy, Sandra J
;  APPLICANT:  Moyses, Christopher
;  TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidn
;  TITLE OF INVENTION:  Response
;  FILE REFERENCE: 2543-1-030
;  CURRENT APPLICATION NUMBER: US/10/601,837
;  CURRENT FILING DATE:  2003-06-23
;  PRIOR APPLICATION NUMBER: PCT/GB01/05777
;  PRIOR FILING DATE: 2001-12-24
;  PRIOR APPLICATION NUMBER: US 60/260392
;  PRIOR FILING DATE: 2000-12-29
;  NUMBER OF SEQ ID NOS: 272
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Ratus No. US20040053309A1vegicus
US-10-601-837-103

  Query Match              3.0%;  Score 32;  DB 12;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1e+04;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         96 GGDFTRGDGT 105
              || |  || |
Db          2 GGPFCAGDAT 11
```

```
RESULT 39
US-10-224-999A-2922
; Sequence 2922, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
;  APPLICANT: Myriad Genetics, Inc.
;  APPLICANT:  Morham, Scott
;  APPLICANT:  Zavitz, Kenton
;  APPLICANT:  Hobden, Adrian
;  TITLE OF INVENTION: Composition and Method for Treating Viral Infection
;  FILE REFERENCE: 5004.01
;  CURRENT APPLICATION NUMBER: US/10/224,999A
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/313,695
;  PRIOR FILING DATE: 2001-08-20
;  NUMBER OF SEQ ID NOS: 3484
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2922
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Hepatitis G virus
US-10-224-999A-2922

  Query Match             3.0%;  Score 32;  DB 14;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1e+04;
  Matches    6;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        185 PLKDVIIADCGK 196
              |   |:|  |||
Db          1 PTAPVVIRRCGK 12


RESULT 40
US-09-991-225-19
; Sequence 19, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
;  TITLE OF INVENTION:  HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-991-225-19

  Query Match             3.0%;  Score 32;  DB 10;  Length 13;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 ITTVKTAWL 154
              :|::::||:
Db          4 VTSIRSAWI 12


RESULT 41
US-09-991-225-38
; Sequence 38, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIC
;  TITLE OF INVENTION:  HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-991-225-38

  Query Match             3.0%;  Score 32;  DB 10;  Length 13;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 ITTVKTAWL 154
              :|::::||:
Db          4 VTSIRSAWI 12


RESULT 42
US-10-369-405-19
; Sequence 19, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11,  AND VARIANTS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0075A CIP
;  CURRENT APPLICATION NUMBER: US/10/369,405
;  CURRENT FILING DATE:  2003-02-14
;  PRIOR APPLICATION NUMBER: U.S. 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: U.S. 09/991,225
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: U.S. 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: U.S. 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-369-405-19

  Query Match             3.0%;  Score 32;  DB 12;  Length 13;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 ITTVKTAWL 154
              :|::::||:
Db          4 VTSIRSAWI 12


RESULT 43
US-10-369-405-38
; Sequence 38, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11,  AND VARIANTS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: D0075A CIP
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; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-405-38

Query Match 3.0%; Score 32; DB 12; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Qy        146 ITTVKTAWL 154
              :|::::||:
Db          4 VTSIRSAWI 12
```

RESULT 44
US-10-224-999A-2931
; Sequence 2931, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2931
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2931

Query Match 3.0%; Score 32; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy        185 PLKDVIIADCGK 196
              |   |:|  |||
Db          2 PTAPVVIRRCGK 13
```

RESULT 45
US-10-224-999A-2932
; Sequence 2932, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2932
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2932

Query Match 3.0%; Score 32; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy        185 PLKDVIIADCGK 196
              |   |:|  |||
Db          1 PTAPVVIRRCGK 12
```

Search completed: August 30, 2004, 11:05:02
Job time : 255.378 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 82.2162 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAAALIAGSVFFLLLP.....VIIADCGKIEVEKPFAIAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	3.5	9	2	US-08-658-639-10	Sequence 10, Appl
2	38	3.5	9	3	US-08-944-604-10	Sequence 10, Appl
3	37	3.4	12	2	US-08-556-597-40	Sequence 40, Appl
4	37	3.4	14	5	PCT-US93-06751-120	Sequence 120, App
5	36	3.3	13	3	US-09-261-855-9	Sequence 9, Appli
6	35	3.2	9	1	US-07-963-324-2	Sequence 2, Appli
7	35	3.2	14	2	US-08-448-418-101	Sequence 101, App
8	35	3.2	14	4	US-09-146-979-101	Sequence 101, App
9	33.5	3.1	12	2	US-08-973-563A-25	Sequence 25, Appl
10	33.5	3.1	12	2	US-08-973-559-25	Sequence 25, Appl
11	33.5	3.1	12	3	US-08-993-235-5	Sequence 5, Appli
12	33.5	3.1	12	4	US-08-993-235-5	Sequence 5, Appli
13	33	3.0	8	1	US-08-482-880-23	Sequence 23, Appl
14	33	3.0	8	2	US-08-273-274-23	Sequence 23, Appl
15	33	3.0	8	2	US-08-475-041-23	Sequence 23, Appl
16	33	3.0	8	2	US-08-484-773-23	Sequence 23, Appl
17	33	3.0	8	2	US-08-361-864-27	Sequence 27, Appl
18	33	3.0	9	2	US-08-335-832-23	Sequence 23, Appl
19	33	3.0	9	2	US-08-753-781-36	Sequence 36, Appl
20	33	3.0	9	3	US-09-141-127-19	Sequence 19, Appl
21	33	3.0	10	2	US-08-658-639-8	Sequence 8, Appli
22	33	3.0	10	3	US-08-944-604-8	Sequence 8, Appli
23	33	3.0	10	4	US-09-269-991B-10	Sequence 10, Appl
24	33	3.0	14	2	US-08-656-906-26	Sequence 26, Appl
25	33	3.0	14	3	US-09-217-847-26	Sequence 26, Appl
26	32.5	3.0	12	2	US-08-973-563A-27	Sequence 27, Appl
27	32.5	3.0	12	2	US-08-973-559-27	Sequence 27, Appl
28	32.5	3.0	12	3	US-08-993-235-7	Sequence 7, Appli
29	32.5	3.0	12	4	US-08-993-235-7	Sequence 7, Appli
30	32.5	3.0	13	3	US-08-394-748A-4	Sequence 4, Appli
31	32.5	3.0	13	3	US-08-916-913A-7	Sequence 7, Appli
32	32.5	3.0	13	4	US-09-591-564-7	Sequence 7, Appli
33	32.5	3.0	13	5	PCT-US95-02478-4	Sequence 4, Appli
34	32	3.0	8	1	US-08-271-830-56	Sequence 56, Appl
35	32	3.0	8	2	US-08-416-870C-15	Sequence 15, Appl
36	32	3.0	9	2	US-08-232-539D-32	Sequence 32, Appl
37	32	3.0	9	3	US-08-466-151-50	Sequence 50, Appl
38	32	3.0	9	4	US-08-466-163B-50	Sequence 50, Appl
39	32	3.0	9	4	US-09-802-096-50	Sequence 50, Appl
40	32	3.0	10	2	US-08-464-025A-9	Sequence 9, Appli
41	32	3.0	10	3	US-08-466-151-17	Sequence 17, Appl
42	32	3.0	10	3	US-08-466-151-46	Sequence 46, Appl
43	32	3.0	10	4	US-08-466-163B-17	Sequence 17, Appl
44	32	3.0	10	4	US-08-466-163B-46	Sequence 46, Appl
45	32	3.0	10	4	US-09-755-630B-33	Sequence 33, Appl

ALIGNMENTS

```
RESULT 1
US-08-658-639-10
; Sequence 10, Application US/08658639
; Patent No. 5914238
;  GENERAL INFORMATION:
;    APPLICANT:  KEESEE, SUSAN
;    APPLICANT:  OBAR, ROBERT
;    APPLICANT:  WU, YING-JYE
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR DETECTION OF
;    TITLE OF INVENTION:  BREAST CANCER
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,639
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEYERS, THOMAS C
;      REGISTRATION NUMBER:  36,989
;      REFERENCE/DOCKET NUMBER:  MTP-021 (8395/24)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-658-639-10

  Query Match             3.5%;  Score 38;  DB 2;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        189 VIIADCGK 196
              |||||||:
Db          1 VIIADCGE 8
```

```
RESULT 2
US-08-944-604-10
; Sequence 10, Application US/08944604
; Patent No. 6218131
;  GENERAL INFORMATION:
;    APPLICANT:  KEESEE, SUSAN
;    APPLICANT:  OBAR, ROBERT
;    APPLICANT:  WU, YING-JYE
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR DETECTION OF
;    TITLE OF INVENTION:  BREAST CANCER
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,604
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEYERS, THOMAS C
;      REGISTRATION NUMBER:  36,989
;      REFERENCE/DOCKET NUMBER:  MTP-021 (8395/24)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-944-604-10

  Query Match             3.5%;  Score 38;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        189 VIIADCGK 196
              |||||||:
Db          1 VIIADCGE 8


RESULT 3
US-08-556-597-40
; Sequence 40, Application US/08556597
; Patent No. 5877155
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Jonathan L.
;    APPLICANT:  Lyle, Vicki A.
;    TITLE OF INVENTION:  MIMOTOPES AND ANTI-MIMOTOPES OF
;    TITLE OF INVENTION:  HUMAN PLATELET GLYCOPROTEIN Ib/IX
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/556,597
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/406,330
;      FILING DATE:  17-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  20884/101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-556-597-40

  Query Match             3.4%;  Score 37;  DB 2;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 8.7e+02;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        156 GKHVVFGKVLEG 167
              |  | ||  ||||
Db          1 GLAVTFGSVLEG 12


RESULT 4
PCT-US93-06751-120
; Sequence 120, Application PC/TUS9306751
;  GENERAL INFORMATION:
;    APPLICANT:  P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
;    TITLE OF INVENTION:  Immunological Conjugates of OMPC and
;    TITLE OF INVENTION:  HIV-Specific Selected Principal Neutralization GXG Epitopes
;    NUMBER OF SEQUENCES:  146
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  P.O. Box 2000
;      CITY:  Rahway
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06751
;      FILING DATE:  19930719
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meredith, Roy D.
;      REGISTRATION NUMBER:  30,777
;      REFERENCE/DOCKET NUMBER:  18614
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-4678
;      TELEFAX:  (908) 594-4720
;      TELEX:  138825
;  INFORMATION FOR SEQ ID NO:  120:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

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;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:  Random Epitope Library Beta
PCT-US93-06751-120

  Query Match              3.4%;  Score 37;  DB 5;  Length 14;
  Best Local Similarity   55.6%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        120 FKLKHYGPG 128
              ::  |||||
Db          3 YRAAHYGPG 11


RESULT 5
US-09-261-855-9
; Sequence 9, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
;  APPLICANT: Ross, Jeffrey
;  TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
;  TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
;  FILE REFERENCE: 960296.95131
;  CURRENT APPLICATION NUMBER: US/09/261,855A
;  CURRENT FILING DATE: 1999-03-03
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus sequence for SEQ ID NOs:3-8.
US-09-261-855-9

  Query Match              3.3%;  Score 36;  DB 3;  Length 13;
  Best Local Similarity   63.6%;  Pred. No. 1.3e+03;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         97 GDFTRGDGTGG 107
              | |  || |  ||
Db          3 GGFGRGGGRGG 13


RESULT 6
US-07-963-324-2
; Sequence 2, Application US/07963324
; Patent No. 5274122
;  GENERAL INFORMATION:
;    APPLICANT:  Marburg, Stephen
;    APPLICANT:  Leanza, William J
;    APPLICANT:  Tolman, Richard L
;    TITLE OF INVENTION:  Acidic Derivatives of Homocysteine
;    TITLE OF INVENTION:  Thiolactone
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/963,324
;      FILING DATE:  19921015
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bencen, Gerard H
;      REGISTRATION NUMBER:  35,746
;      REFERENCE/DOCKET NUMBER:  18787
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3901
;      TELEFAX:  (908)594-4720
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  both
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  /label= Nle
;      OTHER INFORMATION:  /note= "norleucine"
;    FEATURE:
;      NAME/KEY:  Cross-links
;      LOCATION:  2..9
;      OTHER INFORMATION:  /label= cycle
;      OTHER INFORMATION:  /note= "amide bond through Lys epsilon amino"
US-07-963-324-2

  Query Match              3.2%;  Score 35;  DB 1;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        122 LKHYGPG 128
              ||| |||
Db          1 LKHIGPG 7


RESULT 7
US-08-448-418-101
; Sequence 101, Application US/08448418
; Patent No. 5837242
;  GENERAL INFORMATION:
;    APPLICANT:  Holliger, Kaspar-Philipp
;    APPLICANT:  Griffiths, Andrew D
;    APPLICANT:  Hoogenboom, Hendricus RJM
;    APPLICANT:  Malmqvist, Magnus
;    APPLICANT:  Marks, James D
;    APPLICANT:  McGuinness, Brian T
;    APPLICANT:  Pope, Anthony R
;    APPLICANT:  Prospero, Terence D
;    APPLICANT:  Winter, Gregory P
;    TITLE OF INVENTION:  Multivalent and Multispecific Binding
;    TITLE OF INVENTION:  Proteins, Their Manufacture and Use
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall O'Toole Gerstein Murray and Borun
;      STREET:  6300 Sears Tower 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/448,418
;      FILING DATE:  14-MAY-1996
;      CLASSIFICATION:  435
;      CLASSIFICATION:  C12N 15/62, 15/70, C07K 1/00
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB93/02492
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
```

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;      APPLICATION NUMBER:  GB 9225453.1
;      FILING DATE:  04-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9300816.7
;      FILING DATE:  16-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93303614.7
;      FILING DATE:  10-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9319969.3
;      FILING DATE:  22-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32651
;  INFORMATION FOR SEQ ID NO:  101:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide linker
US-08-448-418-101

  Query Match             3.2%;  Score 35;  DB 2;  Length 14;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+03;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         96 GGDFTRGDGTGGKS 109
              ||  : | |:|| |
Db          1 GGGGSGGGGSGGSS 14


RESULT 8
US-09-146-979-101
; Sequence 101, Application US/09146979
; Patent No. 6492123
;  GENERAL INFORMATION:
;    APPLICANT:  Holliger, Kaspar-Philipp
;    APPLICANT:  Griffiths, Andrew D
;    APPLICANT:  Hoogenboom, Hendricus RJM
;    APPLICANT:  Malmqvist, Magnus
;    APPLICANT:  Marks, James D
;    APPLICANT:  McGuinness, Brian T
;    APPLICANT:  Pope, Anthony R
;    APPLICANT:  Prospero, Terence D
;    APPLICANT:  Winter, Gregory P
;    TITLE OF INVENTION:  Multivalent and Multispecific Binding
;    TITLE OF INVENTION:  Proteins, Their Manufacture and Use
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall O'Toole Gerstein Murray and Borun
;      STREET:  6300 Sears Tower 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,979
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/448,418
;      FILING DATE:  14-MAY-1996
;      APPLICATION NUMBER:  PCT/GB93/02492
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9225453.1
;      FILING DATE:  04-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9300816.7
;      FILING DATE:  16-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93303614.7
;      FILING DATE:  10-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9319969.3
;      FILING DATE:  22-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/32651
;  INFORMATION FOR SEQ ID NO:  101:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide linker
US-09-146-979-101

  Query Match             3.2%;  Score 35;  DB 4;  Length 14;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+03;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         96 GGDFTRGDGTGGKS 109
              ||  : | |:|| |
Db          1 GGGGSGGGGSGGSS 14


RESULT 9
US-08-973-563A-25
; Sequence 25, Application US/08973563A
; Patent No. 5885965
;  GENERAL INFORMATION:
;    APPLICANT:  Oppenheim, Frank G.
;    APPLICANT:  Xu, Tao
;    APPLICANT:  Spacciapoli, Peter
;    APPLICANT:  Roberts, F. D.
;    APPLICANT:  Friden, Philip M.
;    TITLE OF INVENTION:  Anti-Fungal D-Amino Acid Histatin-Based
;    TITLE OF INVENTION:  Peptides
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/973,563A
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,273
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  PER95-02A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
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;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  1..12
;      OTHER INFORMATION:  /note= "At least one amino acid
;      OTHER INFORMATION:  must have a D configuration."
US-08-973-563A-25

  Query Match             3.1%;  Score 33.5;  DB 2;  Length 12;
  Best Local Similarity   58.3%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         75 EKGFGYKNSKFH 86
              :: ||||  |||
Db          2 KRHFGYKR-KFH 12


RESULT 10
US-08-973-559-25
; Sequence 25, Application US/08973559
; Patent No. 5912230
;  GENERAL INFORMATION:
;    APPLICANT:  OPPENHEIM, FRANK G.
;    APPLICANT:  XU, TAO
;    APPLICANT:  ROBERTS, F. D.
;    APPLICANT:  SPACCIAPOLI, PETER
;    APPLICANT:  FRIDEN, PHILIP M.
;    TITLE OF INVENTION:  Anti-Fungal and Anti-Bacterial
;    TITLE OF INVENTION:  Histatin-Based Peptides
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/973,559
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,888
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  PER95-01A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-973-559-25

  Query Match             3.1%;  Score 33.5;  DB 2;  Length 12;
  Best Local Similarity   58.3%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         75 EKGFGYKNSKFH 86
              :: ||||  |||
Db          2 KRHFGYKR-KFH 12


RESULT 11
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
;  APPLICANT: OPPENHEIM, FRANK G.
;  APPLICANT: ROBERTS, F. DONALD
;  APPLICANT: XU, TAO
;  APPLICANT: SPACCIAPOLI, PETER
;  TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
;  FILE REFERENCE: 50032/002001
;  CURRENT APPLICATION NUMBER: US/08/993,235
;  CURRENT FILING DATE: 1997-12-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-993-235-5

  Query Match             3.1%;  Score 33.5;  DB 3;  Length 12;
  Best Local Similarity   58.3%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         75 EKGFGYKNSKFH 86
              :: ||||  |||
Db          2 KRHFGYKR-KFH 12


RESULT 12
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
;  APPLICANT: OPPENHEIM, FRANK G.
;  APPLICANT:  ROBERTS, F. DONALD
;  APPLICANT:  XU, TAO
;  APPLICANT:  SPACCIAPOLI, PETER
;  TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
;  FILE REFERENCE: 50032/002001
;  CURRENT APPLICATION NUMBER: US/08/993,235
;  CURRENT FILING DATE:  1997-12-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-993-235-5

  Query Match             3.1%;  Score 33.5;  DB 4;  Length 12;
  Best Local Similarity   58.3%;  Pred. No. 2.1e+03;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy         75 EKGFGYKNSKFH 86
              :: ||||  |||
Db          2 KRHFGYKR-KFH 12


RESULT 13
US-08-482-880-23
; Sequence 23, Application US/08482880
; Patent No. 5736122
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,880
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5736122nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-880-23

  Query Match             3.0%;  Score 33;  DB 1;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 14
US-08-273-274-23
; Sequence 23, Application US/08273274
; Patent No. 5849260
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/273,274
;      FILING DATE:
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/886,752
;      FILING DATE:  21-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5849260nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-273-274-23

  Query Match             3.0%;  Score 33;  DB 2;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 15
US-08-475-041-23
; Sequence 23, Application US/08475041
; Patent No. 5879658
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,041
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5879658nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-M
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-475-041-23

  Query Match             3.0%;  Score 33;  DB 2;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8
```

```
RESULT 16
US-08-484-773-23
; Sequence 23, Application US/08484773
; Patent No. 5968476
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,773
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5968476nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-O
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-484-773-23

  Query Match             3.0%;  Score 33;  DB 2;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 17
US-08-361-864-27
; Sequence 27, Application US/08361864
; Patent No. 5977064
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Multimeric Polyvalent Antithrombotic
;    TITLE OF INVENTION:  Agents
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/361,864
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/955,466A
;      FILING DATE:  19921002
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5977064nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,668
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-361-864-27

  Query Match             3.0%;  Score 33;  DB 2;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 18
US-08-335-832-23
; Sequence 23, Application US/08335832
; Patent No. 5925331
;  GENERAL INFORMATION:
;    APPLICANT:  Dean, Richard T
;    APPLICANT:  Lister-James, John
;    TITLE OF INVENTION:  Technetium-99m Labeled Peptides for
;    TITLE OF INVENTION:  Thrombus Imaging
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti, Ltd.
;      STREET:  10 South Wacker Drive Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,832
;      FILING DATE:  05-JAN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5925331nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  92,216-I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;      TELEX:  910-221-5317
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-335-832-23
```

```
  Query Match             3.0%;  Score 33;  DB 2;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 19
US-08-753-781-36
; Sequence 36, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
;  APPLICANT: Markland Jr., Francis S.
;  APPLICANT: Bush, Larry R.
;  APPLICANT: Swenson, Stephen
;  APPLICANT: Flores Sanchez, Eladio
;  TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
;  FILE REFERENCE: DITI 124
;  CURRENT APPLICATION NUMBER: US/08/753,781C
;  CURRENT FILING DATE: 1996-12-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: peptide
US-08-753-781-36

  Query Match             3.0%;  Score 33;  DB 2;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 20
US-09-141-127-19
; Sequence 19, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:
;  APPLICANT: Dean, Richard T.
;  APPLICANT: Lister-James, John
;  TITLE OF INVENTION: THROMBUS IMAGING AGENTS
;  FILE REFERENCE: DITI 113.1USC1
;  CURRENT APPLICATION NUMBER: US/09/141,127A
;  CURRENT FILING DATE: 1998-08-27
;  EARLIER APPLICATION NUMBER: 08/335,832
;  EARLIER FILING DATE: 1995-01-05
;  EARLIER APPLICATION NUMBER: PCT/US93/04794
;  EARLIER FILING DATE: 1993-05-21
;  EARLIER APPLICATION NUMBER: 07/886,752
;  EARLIER FILING DATE: 1992-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: peptide
US-09-141-127-19

  Query Match             3.0%;  Score 33;  DB 3;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        101 RGDGTGG 107
              |||| ||
Db          2 RGDGGGG 8


RESULT 21
US-08-658-639-8
; Sequence 8, Application US/08658639
; Patent No. 5914238
;  GENERAL INFORMATION:
;    APPLICANT:  KEESEE, SUSAN
;    APPLICANT:  OBAR, ROBERT
;    APPLICANT:  WU, YING-JYE
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR DETECTION OF
;    TITLE OF INVENTION:  BREAST CANCER
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,639
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEYERS, THOMAS C
;      REGISTRATION NUMBER:  36,989
;      REFERENCE/DOCKET NUMBER:  MTP-021 (8395/24)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-658-639-8

  Query Match             3.0%;  Score 33;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+03;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        114 RFPDENFKLK 123
              :| |||| |:
Db          1 KFDDENFILR 10


RESULT 22
US-08-944-604-8
; Sequence 8, Application US/08944604
; Patent No. 6218131
;  GENERAL INFORMATION:
;    APPLICANT:  KEESEE, SUSAN
;    APPLICANT:  OBAR, ROBERT
;    APPLICANT:  WU, YING-JYE
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR DETECTION OF
;    TITLE OF INVENTION:  BREAST CANCER
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
```

```
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02110
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/944,604
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MEYERS, THOMAS C
;       REGISTRATION NUMBER:  36,989
;       REFERENCE/DOCKET NUMBER:  MTP-021 (8395/24)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 248-7000
;       TELEFAX:  (617) 248-7100
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-944-604-8

  Query Match             3.0%;  Score 33;  DB 3;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+03;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        114 RFPDENFKLK 123
              :| |||| |:
Db          1 KFDDENFILR 10


RESULT 23
US-09-269-991B-10
; Sequence 10, Application US/09269991B
; Patent No. 6686333
;   GENERAL INFORMATION:
;       APPLICANT: Kashanchi, Fatah
;                  Sadaie, Mohamad Reza
;                  Brady, John N.
;       TITLE OF INVENTION: Inhibition of HIV Replication Using
;                           Soluble Tat Peptide Analogs
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/269,991B
;            FILING DATE: 07-Sep-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: WO PCT/US97/17704
;            FILING DATE: 02-OCT-1997
;            APPLICATION NUMBER: US 60/027,658
;            FILING DATE: 04-OCT-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Garrett-Wackowski, Eugenia
;            REGISTRATION NUMBER: 37,330
;            REFERENCE/DOCKET NUMBER: 015280-276100US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-269-991B-10

  Query Match             3.0%;  Score 33;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 KKKGPK 33
              ||||||
Db          1 KKKGPK 6


RESULT 24
US-08-656-906-26
; Sequence 26, Application US/08656906
; Patent No. 5972901
;  GENERAL INFORMATION:
;    APPLICANT:  Ferkol Jr., Thomas W.
;    APPLICANT:  Davis, Pamela B.
;    APPLICANT:  Ziady, Assem-Galal
;    TITLE OF INVENTION:  Serpin Enzyme Complex Receptor -
;    TITLE OF INVENTION:  Mediated Gene Transfer
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,906
;      FILING DATE:  03-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/
;      FILING DATE:  03-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO WO 95/25809
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/216,534
;      FILING DATE:  23-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  CASE-02280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
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US-08-656-906-26

Query Match 3.0%; Score 33; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```
Qy         96 GGDFTRGDGTGGKS 109
              ||  : | |:|| |
Db          1 GGGGSGGGGSGGGS 14
```

RESULT 25
US-09-217-847-26
; Sequence 26, Application US/09217847
; Patent No. 6200801
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,847
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,906
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO WO 95/25809
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/216,534
; FILING DATE: 23-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-09-217-847-26

Query Match 3.0%; Score 33; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```
Qy         96 GGDFTRGDGTGGKS 109
              ||  : | |:|| |
Db          1 GGGGSGGGGSGGGS 14
```

RESULT 26

US-08-973-563A-27
; Sequence 27, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note= "At least one amino acid
; OTHER INFORMATION: must have a D configuration."
US-08-973-563A-27

Query Match 3.0%; Score 32.5; DB 2; Length 12;
Best Local Similarity 77.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy         78 FGYKNSKFH 86
              ||||  |||
Db          5 FGYKR-KFH 12
```

RESULT 27
US-08-973-559-27
; Sequence 27, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides

```
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/973,559
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,888
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  PER95-01A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-973-559-27

  Query Match             3.0%;  Score 32.5;  DB 2;  Length 12;
  Best Local Similarity   77.8%;  Pred. No. 2.7e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         78 FGYKNSKFH 86
              ||||  |||
Db          5 FGYKR-KFH 12


RESULT 28
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
;  APPLICANT: OPPENHEIM, FRANK G.
;  APPLICANT: ROBERTS, F. DONALD
;  APPLICANT: XU, TAO
;  APPLICANT: SPACCIAPOLI, PETER
;  TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
;  FILE REFERENCE: 50032/002001
;  CURRENT APPLICATION NUMBER: US/08/993,235
;  CURRENT FILING DATE: 1997-12-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-993-235-7

  Query Match             3.0%;  Score 32.5;  DB 3;  Length 12;
  Best Local Similarity   77.8%;  Pred. No. 2.7e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         78 FGYKNSKFH 86
              ||||  |||
Db          5 FGYKR-KFH 12


RESULT 29
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
;  APPLICANT: OPPENHEIM, FRANK G.
;  APPLICANT:  ROBERTS, F. DONALD
;  APPLICANT:  XU, TAO
;  APPLICANT:  SPACCIAPOLI, PETER
;  TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
;  FILE REFERENCE: 50032/002001
;  CURRENT APPLICATION NUMBER: US/08/993,235
;  CURRENT FILING DATE:  1997-12-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-993-235-7

  Query Match             3.0%;  Score 32.5;  DB 4;  Length 12;
  Best Local Similarity   77.8%;  Pred. No. 2.7e+03;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         78 FGYKNSKFH 86
              ||||  |||
Db          5 FGYKR-KFH 12


RESULT 30
US-08-394-748A-4
; Sequence 4, Application US/08394748A
; Patent No. 6013628
;  GENERAL INFORMATION:
;    APPLICANT:  Skubitz, Amy P.N.
;    APPLICANT:  Furcht Leo T.
;    APPLICANT:  Balles, Mark
;    APPLICANT:  Gregerson, Dale S.
;    APPLICANT:  Agarwal, Anita
;    APPLICANT:  Wright, Martha M.
;    APPLICANT:  Murali, Shobana
;    TITLE OF INVENTION:  Method for Treating Conditions of the Eye
;    TITLE OF INVENTION:  Using Polypeptides
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 No. 6013628west Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/394,748A
;      FILING DATE:  27-FEB-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/203,458
;      FILING DATE:  28-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  600.307US01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
```

```
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      STRAIN:  Hep-III
US-08-394-748A-4

  Query Match             3.0%;  Score 32.5;  DB 3;  Length 13;
  Best Local Similarity   70.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         39 YFDLRI-GDE 47
              |||||: ||:
Db          4 YFDLRLKGDK 13


RESULT 31
US-08-916-913A-7
; Sequence 7, Application US/08916913A
; Patent No. 6121027
;  GENERAL INFORMATION:
;    APPLICANT:  Clapper, David L.
;    APPLICANT:  Swanson, Melvin J.
;    APPLICANT:  Hu, Sheau-Ping
;    APPLICANT:  Amos, Richard A.
;    APPLICANT:  Everson, Terrence P.
;    TITLE OF INVENTION:  LATENT REACTIVE POLYMERS WITH
;    TITLE OF INVENTION:  BIOLOGICALLY ACTIVE MOIETIES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fredrikson & Byron, P.A.
;      STREET:  900 Second Avenue South
;      CITY:  Minneapolis
;      STATE:  Minnesota
;      COUNTRY:  USA
;      ZIP:  55402-3397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows-97
;      SOFTWARE:  ASCII files
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/916,913A
;      FILING DATE:  15 August 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  No. 6121027e
;      FILING DATE:  No. 6121027e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Philip M.
;      REGISTRATION NUMBER:  31,162
;      REFERENCE/DOCKET NUMBER:  9896.116.0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (612) 347-7088
;      TELEFAX:  (612) 347-7077
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 amino acid residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-916-913A-7

  Query Match             3.0%;  Score 32.5;  DB 3;  Length 13;
  Best Local Similarity   70.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         39 YFDLRI-GDE 47
              |||||: ||:
Db          4 YFDLRLKGDK 13


RESULT 32
US-09-591-564-7
; Sequence 7, Application US/09591564
; Patent No. 6514734
;  GENERAL INFORMATION:
;       APPLICANT: Clapper, David L.
;                  Swanson, Melvin J.
;                  Hu, Sheau-Ping
;                  Amos, Richard A.
;                  Everson, Terrence P.
;       TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY
;                           ACTIVE MOIETIES
;       NUMBER OF SEQUENCES: 16
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fredrikson & Byron, P.A.
;            STREET: 900 Second Avenue South
;            CITY: Minneapolis
;            STATE: Minnesota
;            COUNTRY: USA
;            ZIP: 55402-3397
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows-97
;            SOFTWARE: ASCII files
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/591,564
;            FILING DATE: 09-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/916,913
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Goldman, Philip M.
;            REGISTRATION NUMBER: 31,162
;            REFERENCE/DOCKET NUMBER: 9896.116.0
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (612) 347-7088
;            TELEFAX: (612) 347-7077
;  INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 13 amino acid residues
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-591-564-7

  Query Match             3.0%;  Score 32.5;  DB 4;  Length 13;
  Best Local Similarity   70.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         39 YFDLRI-GDE 47
              |||||: ||:
Db          4 YFDLRLKGDK 13


RESULT 33
PCT-US95-02478-4
; Sequence 4, Application PC/TUS9502478
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Method for Treating Conditions
;    TITLE OF INVENTION:  Of the Eye Using Polypeptides
;    NUMBER OF SEQUENCES:  16
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

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;      APPLICATION NUMBER:  PCT/US95/02478
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/203,458
;      FILING DATE:  28-FEB-1994
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      STRAIN:  Hep-III
PCT-US95-02478-4

  Query Match              3.0%;  Score 32.5;  DB 5;  Length 13;
  Best Local Similarity   70.0%;  Pred. No. 3e+03;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         39 YFDLRI-GDE 47
              |||||: ||:
Db          4 YFDLRLKGDK 13


RESULT 34
US-08-271-830-56
; Sequence 56, Application US/08271830
; Patent No. 5510332
;  GENERAL INFORMATION:
;    APPLICANT:  Kogan, Timothy P.
;    APPLICANT:  Ren, Kaijun
;    APPLICANT:  Vanderslice, Peter
;    APPLICANT:  Beck, Pamela J.
;    TITLE OF INVENTION:  A PROCESS OF INHIBITING THE BINDING OF THE
;    TITLE OF INVENTION:  INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
;    TITLE OF INVENTION:  LINEAR PEPTIDES THEREFOR
;    NUMBER OF SEQUENCES:  102
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dressler, Goldsmith, Shore & Milnamow, Ltd.
;      STREET:  180 No. 5510332th Stetson, Suite 4700
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,830
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5510332thrup, Thomas E.
;      REGISTRATION NUMBER:  33,268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312)616-5400
;      TELEFAX:  (312)616-5460
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  8
;      OTHER INFORMATION:  /label= Xaa
;      OTHER INFORMATION:  /note= "Xaa=Pro-NH2."
US-08-271-830-56

  Query Match              3.0%;  Score 32;  DB 1;  Length 8;
  Best Local Similarity   57.1%;  Pred. No. 3e+05;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         126 GPGWVSM 132
               ||||: :
Db           1 GPGWLDV 7


RESULT 35
US-08-416-870C-15
; Sequence 15, Application US/08416870C
; Patent No. 5824862
;  GENERAL INFORMATION:
;    APPLICANT:  HIYOSHI, TORU
;    APPLICANT:  MINE, TOSHIKI
;    APPLICANT:  KASAOKA, KEISUKE
;    APPLICANT:  TYSON, ROBERT HUW
;    APPLICANT:  PAGE, ANTHONY MILES JOHN
;    TITLE OF INVENTION:  DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
;    TITLE OF INVENTION:  1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR
;    TITLE OF INVENTION:  SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH, LLP
;      STREET:  PO BOX 747
;      CITY:  FALL CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/416,870C
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  760-195P(PCT)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-416-870C-15

  Query Match              3.0%;  Score 32;  DB 2;  Length 8;
  Best Local Similarity   83.3%;  Pred. No. 3e+05;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          62 PKTVDN 67
               |||:||
Db           1 PKTIDN 6


RESULT 36
US-08-232-539D-32
; Sequence 32, Application US/08232539D
; Patent No. 5965709
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Jardieu, Paula M.
;    TITLE OF INVENTION:  IgE Antagonists
;    NUMBER OF SEQUENCES:  60
```

```
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  1 DNA Way
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,539D
;       FILING DATE:  21-Apr-1994
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/178583
;       FILING DATE:  07-JAN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/744768
;       FILING DATE:  14-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Svoboda, Craig G.
;       REGISTRATION NUMBER:  39,044
;       REFERENCE/DOCKET NUMBER:  P0718P3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-1489
;       TELEFAX:  650/952-9881
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-232-539D-32

  Query Match             3.0%;  Score 32;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8


RESULT 37
US-08-466-151-50
; Sequence 50, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;     APPLICANT:  Jardieu, Paula M.
;     APPLICANT:  Presta, Leonard G.
;     TITLE OF INVENTION:  Immunoglobulin Variants
;     NUMBER OF SEQUENCES:  65
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  1 DNA Way
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/466,151
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/466163
;       FILING DATE:  06-Jun-1995
;       APPLICATION NUMBER:  08/405617
;       FILING DATE:  15-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/185899
;       FILING DATE:  26-JAN-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/879495
;       FILING DATE:  07-MAY-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/744768
;       FILING DATE:  14-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Svoboda, Craig G.
;       REGISTRATION NUMBER:  39,044
;       REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650/225-1489
;       TELEFAX:  650/952-9881
;   INFORMATION FOR SEQ ID NO:  50:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  9 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-466-151-50

  Query Match             3.0%;  Score 32;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8


RESULT 38
US-08-466-163B-50
; Sequence 50, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-08-466-163B-50

  Query Match             3.0%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8


RESULT 39
US-09-802-096-50
```

; Sequence 50, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-096-50

Query Match 3.0%; Score 32; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          4 WLDGK 8
```

RESULT 40
US-08-464-025A-9
; Sequence 9, Application US/08464025A
; Patent No. 5994514
; GENERAL INFORMATION:
; APPLICANT: Jardieu et al.
; TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,025A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-464-025A-9

Query Match 3.0%; Score 32; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9
```

RESULT 41
US-08-466-151-17
; Sequence 17, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-17

Query Match 3.0%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9
```

```
RESULT 42
US-08-466-151-46
; Sequence 46, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;    APPLICANT:  Jardieu, Paula M.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,151
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/466163
;      FILING DATE:  06-Jun-1995
;      APPLICATION NUMBER:  08/405617
;      FILING DATE:  15-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185899
;      FILING DATE:  26-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/879495
;      FILING DATE:  07-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-466-151-46

  Query Match             3.0%;  Score 32;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 43
US-08-466-163B-17
; Sequence 17, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-466-163B-17

  Query Match             3.0%;  Score 32;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 44
US-08-466-163B-46
; Sequence 46, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 46
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-08-466-163B-46

  Query Match             3.0%;  Score 32;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WLDGK 157
              |||||
Db          5 WLDGK 9


RESULT 45
US-09-755-630B-33
; Sequence 33, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;  CURRENT APPLICATION NUMBER: US/09/755,630B
```

; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-33

Query Match 3.0%; Score 32; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy        201 KPFAIAKE 208
              :||| |||
Db          3 RPFAAAKE 10
```

Search completed: August 30, 2004, 10:57:21
Job time : 83.2162 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIKDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	92.3	9	3	AAY69962	Aay69962 Human cyc
2	36	92.3	9	3	AAY69960	Aay69960 Human cyc
3	36	92.3	9	3	AAY69921	Aay69921 Human cyc
4	36	92.3	9	4	AAB46946	Aab46946 Human cyc
5	36	92.3	9	4	AAB46930	Aab46930 Human cyc
6	36	92.3	9	4	AAG68088	Aag68088 Antitumou
7	36	92.3	9	5	ABG79075	Abg79075 Human Cyp
8	36	92.3	9	6	ABR84373	Abr84373 Human Cyp
9	36	92.3	9	7	ADC17701	Adc17701 Cyclophil
10	36	92.3	9	8	ADG89641	Adg89641 Class I H
11	28	71.8	9	5	ABG94771	Abg94771 Replikin
12	28	71.8	9	5	ABG94772	Abg94772 Replikin
13	28	71.8	9	6	ABU57321	Abu57321 Replikin
14	28	71.8	9	6	ABU57322	Abu57322 Replikin
15	28	71.8	9	7	ADD88394	Add88394 Tumour vi
16	28	71.8	9	7	ADD88395	Add88395 Tumour vi
17	28	71.8	9	7	ADG18172	Adg18172 Tumour vi
18	28	71.8	9	7	ADG18173	Adg18173 Tumour vi
19	27	69.2	12	2	AAW92359	Aaw92359 CYP2B1 im
20	25	64.1	7	8	ADF66836	Adf66836 Human his
21	25	64.1	10	8	ADF66861	Adf66861 Murine hi
22	25	64.1	10	8	ADF66867	Adf66867 Human his
23	25	64.1	11	3	AAY69924	Aay69924 Human cyc
24	25	64.1	12	8	ADO33999	Ado33999 Fucosyltr
25	24	61.5	9	5	ABG32837	Abg32837 PP2AA-bin
26	24	61.5	9	5	ABG32836	Abg32836 PP2AA-bin
27	23	59.0	10	2	AAR96521	Aar96521 Hepatitis
28	23	59.0	10	8	ADP26227	Adp26227 Plasmodiu
29	23	59.0	11	2	AAR48203	Aar48203 Human pho
30	23	59.0	11	2	AAW67692	Aaw67692 LXXLL sig
31	23	59.0	11	4	AAB82292	Aab82292 Phosphory
32	23	59.0	11	6	ABU57332	Abu57332 Replikin
33	23	59.0	11	7	ADD88405	Add88405 Transform
34	23	59.0	11	7	ADG18183	Adg18183 Transform
35	23	59.0	12	1	AAP93365	Aap93365 Amino aci
36	23	59.0	12	2	AAY43067	Aay43067 GRIP1 nuc
37	22	56.4	9	2	AAW82306	Aaw82306 Transport
38	22	56.4	9	3	AAB28435	Aab28435 Bacillus
39	22	56.4	9	8	ADN68529	Adn68529 Human 273
40	22	56.4	10	2	AAR92146	Aar92146 Porphyrom
41	22	56.4	10	5	ABB74381	Abb74381 Karyophil
42	22	56.4	12	2	AAR35255	Aar35255 D32.39 an
43	22	56.4	12	2	AAR56723	Aar56723 Random pe
44	22	56.4	12	2	AAR91471	Aar91471 D32.39 mo
45	22	56.4	12	2	AAW25253	Aaw25253 Antibody

ALIGNMENTS

RESULT 1
AAY69962
ID AAY69962 standard; peptide; 9 AA.
XX
AC AAY69962;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #42.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| ||||||

```
Db          1 KYHRVIKD 8


RESULT 2
AAY69960
ID   AAY69960 standard; peptide; 9 AA.
XX
AC   AAY69960;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #40.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Tyr, Met, Trp
FT   Misc-difference 9
FT                   /label= Phe, Leu, Ile, Trp, Met
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 10; Page 59; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             92.3%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              ||||||||
Db          1 KXHRVIKD 8


RESULT 3
AAY69921
ID   AAY69921 standard; peptide; 9 AA.
XX
AC   AAY69921;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #1.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 49; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             92.3%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | |||:||
Db          1 KFHRVIKD 8


RESULT 4
AAB46946
ID   AAB46946 standard; peptide; 9 AA.
XX
AC   AAB46946;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 19; 25pp; English.
```

```
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;

  Query Match             92.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KYHRVIKD 8


RESULT 5
AAB46930
ID   AAB46930 standard; peptide; 9 AA.
XX
AC   AAB46930;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 15; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;

  Query Match             92.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KFHRVIKD 8


RESULT 6
AAG68088
ID   AAG68088 standard; peptide; 9 AA.
XX
AC   AAG68088;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Antitumour peptide cyclophilin B 84-92.
XX
KW   Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW   tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW   cyclophilin B gene; HLA-A2402.
XX
OS   Homo sapiens.
XX
PN   JP2001245675-A.
XX
PD   11-SEP-2001.
XX
PF   25-DEC-2000; 2000JP-00393047.
XX
PR   28-DEC-1999;   99JP-00374322.
XX
PA   (ITOY/) ITO Y.
XX
DR   WPI; 2001-610076/70.
XX
PT   New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT   lymphocytes and for treating cancer.
XX
PS   Claim 8; Page 2; 14pp; Japanese.
XX
CC   The present invention describes peptides recognising cancer cells with
CC   tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC   cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC   sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC   mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC   the above mentioned sequences; and (4) peptides with one or more deleted,
CC   substituted, added or inserted amino acid(s) of the above mentioned
CC   sequences, particularly those having recognising property due to HLA-
CC   A2402 binding CTL, especially having at least 5 amino acids, used for
CC   medicine, particularly anticancer agents, derived from antitumour
CC   antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC   genes. The antitumour peptides have cytostatic activities. The peptides
CC   are used for the treatment of cancer. The peptides cause activation of
CC   CTL in cancer patients. The present sequence represents a peptide from
CC   the present invention
XX
SQ   Sequence 9 AA;

  Query Match             92.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KFHRVIKD 8
```

RESULT 7
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 9 AA;

```
  Query Match             92.3%;  Score 36;  DB 5;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KFHRVIKD 8
```

RESULT 8
ABR84373
ID ABR84373 standard; peptide; 9 AA.
XX
AC ABR84373;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:23.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

```
  Query Match             92.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KFHRVIKD 8
```

RESULT 9
ADC17701
ID ADC17701 standard; peptide; 9 AA.
XX
AC ADC17701;

XX
DT 18-DEC-2003 (first entry)
XX
DE Cyclophilin B protein amino acids 84-92.
XX
KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX
PN WO2003020306-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002WO-JP008641.
XX
PR 29-AUG-2001; 2001JP-00260046.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Yamada A;
XX
DR WPI; 2003-300831/29.
XX
PT Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 1; 49pp; Japanese.
XX
CC The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet dos not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 84-92 of the cyclophilin B protein.
XX
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 7; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| ||||||
Db 1 KFHRVIKD 8

RESULT 10
ADG89641
ID ADG89641 standard; peptide; 9 AA.
XX
AC ADG89641;
XX
DT 11-MAR-2004 (first entry)
XX
DE Class I HLA-restricted widely expressed antigen #6.
XX
KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS Unidentified.
XX
PN WO2003100027-A2.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-US016736.
XX
PR 28-MAY-2002; 2002US-0383530P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2004-035134/03.
XX
PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
PS Disclosure; SEQ ID NO 84; 137pp; English.
XX
CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted widely expressed
CC antigen.
XX
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 8; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| ||||||
Db 1 KFHRVIKD 8

RESULT 11
ABG94771
ID ABG94771 standard; peptide; 9 AA.
XX
AC ABG94771;
XX
DT 02-DEC-2002 (first entry)
XX
DE Replikin sequence identiied by the 3-point recognition method #44.
XX
KW Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
KW Surface Antigen S Precursor Protein.
XX
OS Polyoma virus.
XX
PN US2002120106-A1.
XX
PD 29-AUG-2002.
XX
PF 26-OCT-2001; 2001US-00984056.
XX
PR 04-SEP-1998; 98US-00146755.
PR 27-MAR-2001; 2001US-00817144.
PR 27-MAR-2001; 2001US-0278761P.
PR 09-JUL-2001; 2001US-0303396P.
XX
PA (BOGO/) BOGOCH S.
PA (BOGO/) BOGOCH E S.
XX
PI Bogoch S, Bogoch ES;
XX
DR WPI; 2002-691212/74.
XX
PT Isolated Bacillus anthracis and small pox virus peptides (I), also known
PT as replikins, useful for formulating vaccines for treating anthrax or
PT small pox, comprise 7 to 50 amino acids.

XX
PS Disclosure; Page 3; 16pp; English.
XX
CC The invention relates to isolated Bacillus anthracis and small pox virus
CC peptides, also known as replikins, comprising 7 to 50 amino acids
CC including at least one lysine residue located six to ten residues from a
CC second lysine residue, at least one histidine residue, and at least 6%
CC lysine residues. The peptides were identified using the 3-point-
CC recognition method and based on the replikin sequence isolated from
CC glioblastoma cells malignin peptide which is of non-human origin. Also
CC included are anti-replikin antibodies (or antibody cocktail), a method of
CC stimulating the immune system of a subject to produce antibodies to
CC Bacillus anthracis or small pox comprising administering an effective
CC amount of at least one or more Bacillus anthracis or small pox replikin
CC and an antisense nucleic acid molecule complementary to a mRNA encoding a
CC Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-
CC 107) comprising a replikin sequence, an antisense nucleic acid molecule
CC complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.
CC Surface Antigen S Precursor Protein comprising a replikin sequence. The
CC peptides are useful for stimulating the immune system of a subject to
CC produce antibodies that bind specifically to Anthrax or small pox
CC polypeptides containing a replikin sequence. The peptides are useful for
CC generating antibodies that can be used in the treatment and/or prevention
CC of anthrax or small pox. The peptides are also useful for formulating
CC vaccines for treating anthrax or small pox. The present sequence is a
CC replikin sequence isolated by the 3-point-recognition system and sharing
CC structural similarity with the replikin sequence isolated from
CC glioblastoma cells malignin
XX
SQ Sequence 9 AA;

```
  Query Match             71.8%;  Score 28;  DB 5;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 12
ABG94772
ID ABG94772 standard; peptide; 9 AA.
XX
AC ABG94772;
XX
DT 02-DEC-2002 (first entry)
XX
DE Replikin sequence identiied by the 3-point recognition method #45.
XX
KW Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
KW Surface Antigen S Precursor Protein.
XX
OS Polyoma virus.
XX
PN US2002120106-A1.
XX
PD 29-AUG-2002.
XX
PF 26-OCT-2001; 2001US-00984056.
XX
PR 04-SEP-1998; 98US-00146755.
PR 27-MAR-2001; 2001US-00817144.
PR 27-MAR-2001; 2001US-0278761P.
PR 09-JUL-2001; 2001US-0303396P.
XX
PA (BOGO/) BOGOCH S.
PA (BOGO/) BOGOCH E S.
XX
PI Bogoch S, Bogoch ES;
XX
DR WPI; 2002-691212/74.

XX
PT Isolated Bacillus anthracis and small pox virus peptides (I), also known
PT as replikins, useful for formulating vaccines for treating anthrax or
PT small pox, comprise 7 to 50 amino acids.
XX
PS Disclosure; Page 3; 16pp; English.
XX
CC The invention relates to isolated Bacillus anthracis and small pox virus
CC peptides, also known as replikins, comprising 7 to 50 amino acids
CC including at least one lysine residue located six to ten residues from a
CC second lysine residue, at least one histidine residue, and at least 6%
CC lysine residues. The peptides were identified using the 3-point-
CC recognition method and based on the replikin sequence isolated from
CC glioblastoma cells malignin peptide which is of non-human origin. Also
CC included are anti-replikin antibodies (or antibody cocktail), a method of
CC stimulating the immune system of a subject to produce antibodies to
CC Bacillus anthracis or small pox comprising administering an effective
CC amount of at least one or more Bacillus anthracis or small pox replikin
CC and an antisense nucleic acid molecule complementary to a mRNA encoding a
CC Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-
CC 107) comprising a replikin sequence, an antisense nucleic acid molecule
CC complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.
CC Surface Antigen S Precursor Protein comprising a replikin sequence. The
CC peptides are useful for stimulating the immune system of a subject to
CC produce antibodies that bind specifically to Anthrax or small pox
CC polypeptides containing a replikin sequence. The peptides are useful for
CC generating antibodies that can be used in the treatment and/or prevention
CC of anthrax or small pox. The peptides are also useful for formulating
CC vaccines for treating anthrax or small pox. The present sequence is a
CC replikin sequence isolated by the 3-point-recognition system and sharing
CC structural similarity with the replikin sequence isolated from
CC glioblastoma cells malignin
XX
SQ Sequence 9 AA;

```
  Query Match             71.8%;  Score 28;  DB 5;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 13
ABU57321
ID ABU57321 standard; peptide; 9 AA.
XX
AC ABU57321;
XX
DT 08-APR-2003 (first entry)
XX
DE Replikin peptide sequence #61.
XX
KW Replikin; immunostimulant; vaccine; recognin.
XX
OS Polyomavirus sp.
XX
PN US2002151677-A1.
XX
PD 17-OCT-2002.
XX
PF 26-OCT-2001; 2001US-00984057.
XX
PR 27-MAR-2001; 2001US-0278761P.
PR 09-JUL-2001; 2001US-0303396P.
XX
PA (BOGO/) BOGOCH S.
PA (BOGO/) BOGOCH E S.
XX
PI Bogoch S, Bogoch ES;
XX
DR WPI; 2003-182530/18.

XX
PT New replikins or recognin peptides, useful for stimulating the immune
PT system, and for targeting, labeling or destroying replikin-containing
PT organisms.
XX
PS Claim 78; Page 3; 17pp; English.
XX
CC The invention describes an isolated replikin or recognin peptide (I)
CC comprising 7-50 amino acids including at least one lysine residue located
CC 6 to 10 residues from a second lysine residue, at least one histidine
CC residue and at least 6% lysine residues. The peptides are useful for
CC stimulating the immune system, and for targeting, labelling or destroying
CC replikin-containing organisms. The computer-readable mediums are useful
CC for identifying a protein or peptide containing a replikin or recognin
CC sequence. This is the amino acid sequence of a replikin peptide
CC identified in the invention
XX
SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 14
ABU57322
ID ABU57322 standard; peptide; 9 AA.
XX
AC ABU57322;
XX
DT 08-APR-2003 (first entry)
XX
DE Replikin peptide sequence #62.
XX
KW Replikin; immunostimulant; vaccine; recognin.
XX
OS Polyomavirus sp.
XX
PN US2002151677-A1.
XX
PD 17-OCT-2002.
XX
PF 26-OCT-2001; 2001US-00984057.
XX
PR 27-MAR-2001; 2001US-0278761P.
PR 09-JUL-2001; 2001US-0303396P.
XX
PA (BOGO/) BOGOCH S.
PA (BOGO/) BOGOCH E S.
XX
PI Bogoch S, Bogoch ES;
XX
DR WPI; 2003-182530/18.
XX
PT New replikins or recognin peptides, useful for stimulating the immune
PT system, and for targeting, labeling or destroying replikin-containing
PT organisms.
XX
PS Claim 79; Page 3; 17pp; English.
XX
CC The invention describes an isolated replikin or recognin peptide (I)
CC comprising 7-50 amino acids including at least one lysine residue located
CC 6 to 10 residues from a second lysine residue, at least one histidine
CC residue and at least 6% lysine residues. The peptides are useful for
CC stimulating the immune system, and for targeting, labelling or destroying
CC replikin-containing organisms. The computer-readable mediums are useful
CC for identifying a protein or peptide containing a replikin or recognin
CC sequence. This is the amino acid sequence of a replikin peptide
CC identified in the invention
XX
SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 15
ADD88394
ID ADD88394 standard; peptide; 9 AA.
XX
AC ADD88394;
XX
DT 29-JAN-2004 (first entry)
XX
DE Tumour viral Replikin #14.
XX
KW vaccine; gene therapy; malaria; influenza; Replikin; haemagglutinin.
XX
OS Polyomavirus.
XX
PN US2003180328-A1.
XX
PD 25-SEP-2003.
XX
PF 26-MAR-2002; 2002US-00105232.
XX
PR 27-MAR-2001; 2001US-0278761P.
PR 09-JUL-2001; 2001US-0303396P.
PR 26-OCT-2001; 2001US-00984057.
XX
PA (BOGO/) BOGOCH S.
PA (BOGO/) BOGOCH E S.
XX
PI Bogoch S, Bogoch ES;
XX
DR WPI; 2003-852213/79.
XX
PT New Replikin peptides of Plasmodium falciparum or influenza virus, useful
PT for diagnosing, preventing or treating influenza virus infection or
PT malaria.
XX
PS Disclosure; SEQ ID NO 61; 136pp; English.
XX
CC The invention relates to an isolated Plasmodium falciparum peptide or an
CC influenza virus peptide. The composition and methods are useful in
CC diagnosing, preventing or treating influenza virus infection or malaria.
CC Also disclosed is an influenza virus vaccine comprising at least one
CC isolated Replikin present in the haemagglutinin protein of an emerging
CC strain of influenza virus and a pharmaceutical carrier and/or adjuvant
CC and a malaria vaccine comprising at least one isolated P. falciparum
CC Replikin and a pharmaceutical carrier. The present sequence represents
CC the amino acid sequence of a Replikin sequence.
XX
SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
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Search completed: October 21, 2004, 07:20:58
Job time : 86 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
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Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIKDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	69.2	12	2	US-08-471-286-1	Sequence 1, Appli
2	25	64.1	11	1	US-08-378-761A-68	Sequence 68, Appl
3	25	64.1	11	1	US-08-485-286-68	Sequence 68, Appl
4	25	64.1	12	4	US-10-037-311B-16	Sequence 16, Appl
5	23	59.0	10	3	US-08-836-075A-204	Sequence 204, App
6	22	56.4	11	4	US-09-418-780A-14	Sequence 14, Appl
7	22	56.4	11	4	US-09-418-780A-22	Sequence 22, Appl
8	22	56.4	12	1	US-07-778-233B-29	Sequence 29, Appl
9	22	56.4	12	1	US-07-963-321-29	Sequence 29, Appl
10	22	56.4	12	1	US-08-290-641-29	Sequence 29, Appl
11	22	56.4	12	1	US-08-548-540-29	Sequence 29, Appl
12	22	56.4	12	5	PCT-US96-09809-29	Sequence 29, Appl
13	21	53.8	10	1	US-08-397-633A-93	Sequence 93, Appl
14	21	53.8	10	3	US-09-105-839D-72	Sequence 72, Appl
15	21	53.8	10	4	US-09-344-040C-114	Sequence 114, App
16	21	53.8	10	4	US-09-833-039A-114	Sequence 114, App
17	21	53.8	12	1	US-07-778-233B-28	Sequence 28, Appl
18	21	53.8	12	1	US-07-778-233B-57	Sequence 57, Appl
19	21	53.8	12	1	US-07-963-321-28	Sequence 28, Appl
20	21	53.8	12	1	US-07-963-321-57	Sequence 57, Appl
21	21	53.8	12	1	US-08-290-641-28	Sequence 28, Appl
22	21	53.8	12	1	US-08-290-641-57	Sequence 57, Appl
23	21	53.8	12	1	US-08-548-540-28	Sequence 28, Appl
24	21	53.8	12	1	US-08-548-540-57	Sequence 57, Appl
25	21	53.8	12	5	PCT-US96-09809-28	Sequence 28, Appl
26	21	53.8	12	5	PCT-US96-09809-57	Sequence 57, Appl
27	20	51.3	7	4	US-09-057-363C-26	Sequence 26, Appl
28	20	51.3	7	4	US-09-265-107-26	Sequence 26, Appl
29	20	51.3	8	3	US-08-893-534A-46	Sequence 46, Appl
30	20	51.3	8	3	US-08-996-679-46	Sequence 46, Appl
31	20	51.3	8	3	US-09-115-395-76	Sequence 76, Appl
32	20	51.3	8	3	US-09-507-102-46	Sequence 46, Appl
33	20	51.3	8	3	US-09-250-059-48	Sequence 48, Appl
34	20	51.3	8	3	US-09-248-074-48	Sequence 48, Appl
35	20	51.3	8	4	US-09-357-717-30	Sequence 30, Appl
36	20	51.3	8	4	US-09-458-870-48	Sequence 48, Appl
37	20	51.3	8	4	US-09-248-015-60	Sequence 60, Appl
38	20	51.3	8	4	US-09-544-782-48	Sequence 48, Appl
39	20	51.3	8	4	US-09-234-395-314	Sequence 314, App
40	20	51.3	8	4	US-09-305-928-314	Sequence 314, App
41	20	51.3	8	4	US-10-058-821-30	Sequence 30, Appl
42	20	51.3	10	2	US-08-556-597-122	Sequence 122, App
43	20	51.3	10	3	US-08-836-075A-205	Sequence 205, App
44	20	51.3	11	6	5210075-43	Patent No. 5210075
45	20	51.3	12	3	US-08-742-243-6	Sequence 6, Appli

ALIGNMENTS

```
RESULT 1
US-08-471-286-1
; Sequence 1, Application US/08471286
; Patent No. 5866688
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Hyesook
;    APPLICANT:  Charnecki, Jonathan
;    APPLICANT:  Putt, David A.
;    APPLICANT:  Kim, Edward Y.
;    TITLE OF INVENTION:  PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
;    TITLE OF INVENTION:  AGAINST CYTOCHROME P450
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099-4390
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,286
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-301 (Oxford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-471-286-1

  Query Match             69.2%;  Score 27;  DB 2;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 17;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              ||| ||
Db          7 HRVTKD 12
```

```
RESULT 2
US-08-378-761A-68
; Sequence 68, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-68

  Query Match             64.1%;  Score 25;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 41;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              |  ||:||
Db          3 KKARVVKD 10


RESULT 3
US-08-485-286-68
; Sequence 68, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-68

  Query Match             64.1%;  Score 25;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 41;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              |  ||:||
Db          3 KKARVVKD 10


RESULT 4
US-10-037-311B-16
; Sequence 16, Application US/10037311B
; Patent No. 6747190
; GENERAL INFORMATION:
;  APPLICANT: MICHIGAN STATE UNIVERSITY
;  TITLE OF INVENTION: XYLOGLUCAN FUCOSYLTRANSFERASES
;  FILE REFERENCE: MS00-001C2
;  CURRENT APPLICATION NUMBER: US/10/037,311B
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER: US60/117,555
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Cross-species
US-10-037-311B-16

  Query Match             64.1%;  Score 25;  DB 4;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 45;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |:||:|
Db          6 HQVIRD 11


RESULT 5
US-08-836-075A-204
; Sequence 204, Application US/08836075A
; Patent No. 6180768
;  GENERAL INFORMATION:
;    APPLICANT:  MAERTENS, GEERT
;    APPLICANT:  STUYVER, LIEVEN
```

```
;    TITLE OF INVENTION:  NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
;    TITLE OF INVENTION:  AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
;    TITLE OF INVENTION:  AGENTS
;    NUMBER OF SEQUENCES:  207
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word 6.0 / ASCII text output
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,075A
;      FILING DATE:  21 Apr 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/04155
;      FILING DATE:  23 Oct 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94870166.9
;      FILING DATE:  21 Oct 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95870076.7
;      FILING DATE:  28 Jun 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KAMMERER, PATRICIA A.
;      REGISTRATION NUMBER:  29,775
;      REFERENCE/DOCKET NUMBER:  INNS:004
;  INFORMATION FOR SEQ ID NO:  204:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-075A-204

  Query Match             59.0%;  Score 23;  DB 3;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 99;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | |:| :|
Db          3 KYHQVTQD 10


RESULT 6
US-09-418-780A-14
; Sequence 14, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/09/418,780A
;  CURRENT FILING DATE:  1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-418-780A-14

  Query Match             56.4%;  Score 22;  DB 4;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |::||
Db          2 HKIIK 6


RESULT 7
US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/09/418,780A
;  CURRENT FILING DATE:  1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-418-780A-22

  Query Match             56.4%;  Score 22;  DB 4;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |::||
Db          2 HKIIK 6


RESULT 8
US-07-778-233B-29
; Sequence 29, Application US/07778233B
; Patent No. 5270170
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/778,233B
;      FILING DATE:  19911016
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11509-50
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  12 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  26 4 0.8
US-07-778-233B-29

  Query Match             56.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |||::
Db          6 HRVVR 10


RESULT 9
US-07-963-321-29
; Sequence 29, Application US/07963321
; Patent No. 5338665
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    APPLICANT:  Stemmer, Willem P.C.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/963,321
;      FILING DATE:  19921015
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/778,223
;      FILING DATE:  16-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11509-50-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  26 4 0.8
US-07-963-321-29

  Query Match             56.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |||::
Db          6 HRVVR 10


RESULT 10
US-08-290-641-29
; Sequence 29, Application US/08290641
; Patent No. 5498530
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    APPLICANT:  Stemmer, Willem P.C.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,641
;      FILING DATE:  15-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,321
;      FILING DATE:  15-OCT-1992
;      APPLICATION NUMBER:  US 07/778,223
;      FILING DATE:  16-OCT-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11509-50-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  26 4 0.8
US-08-290-641-29

  Query Match             56.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |||::
Db          6 HRVVR 10


RESULT 11
US-08-548-540-29
; Sequence 29, Application US/08548540
; Patent No. 5733731
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    APPLICANT:  Stemmer, Willem P.C.
;    APPLICANT:  Gates, Christian M.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  162
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/548,540
;      FILING DATE:  26-OCT-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/290,641
;      FILING DATE:  15-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,321
;      FILING DATE:  15-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  16528J-001240US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  26 4 0.8
US-08-548-540-29

  Query Match             56.4%;  Score 22;  DB 1;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |||::
Db          6 HRVVR 10


RESULT 12
PCT-US96-09809-29
; Sequence 29, Application PC/TUS9609809
;  GENERAL INFORMATION:
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Cull, Millard G.
;    APPLICANT:  Miller, Jeff F.
;    APPLICANT:  Stemmer, Willem P.C.
;    APPLICANT:  Gates, Christian M.
;    TITLE OF INVENTION:  Peptide Library and Screening Method
;    NUMBER OF SEQUENCES:  162
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09809
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/548,540
;      FILING DATE:  26-OCT-1995
;      APPLICATION NUMBER:  US 08/290,641
;      FILING DATE:  15-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,321
;      FILING DATE:  15-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  16528J-001240US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      CLONE:  26 4 0.8
PCT-US96-09809-29

  Query Match             56.4%;  Score 22;  DB 5;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 1.9e+02;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |||::
Db          6 HRVVR 10


RESULT 13
US-08-397-633A-93
; Sequence 93, Application US/08397633A
; Patent No. 5773577
;  GENERAL INFORMATION:
;    APPLICANT:  Cappello, Joseph
;    TITLE OF INVENTION:  PRODUCTS COMPRISING SUBSTRATESCAPABLE
;    TITLE OF INVENTION:  OF ENZYMATIC CROSS-LINKING
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,633A
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20,015
;      REFERENCE/DOCKET NUMBER:  A-58848-1/BIR PROP-011-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  93:
;    SEQUENCE CHARACTERISTICS:
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; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-93

  Query Match 53.8%; Score 21; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred. No. 2.6e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HRVI 6
      ||||
Db 6 HRVI 9

RESULT 14
US-09-105-839D-72
; Sequence 72, Application US/09105839D
; Patent No. 6287756
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Sahin, Ugur
; APPLICANT: Gure, Ali
; APPLICANT: Old, Lloyd J
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
; TITLE OF INVENTION: Expression of an SSX gene
; FILE REFERENCE: LUD 5556
; CURRENT APPLICATION NUMBER: US/09/105,839D
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-105-839D-72

  Query Match 53.8%; Score 21; DB 3; Length 10;
  Best Local Similarity 50.0%; Pred. No. 2.6e+02;
  Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVI 6
      : ||:|
Db 5 RLHRII 10

RESULT 15
US-09-344-040C-114
; Sequence 114, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 114
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-114

  Query Match 53.8%; Score 21; DB 4; Length 10;
  Best Local Similarity 50.0%; Pred. No. 2.6e+02;
  Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVI 6
      : ||:|
Db 5 RLHRII 10

Search completed: October 21, 2004, 07:29:28
Job time : 22.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIKDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	46.2	10	2	PC4374	telomeric and tetr
2	16	41.0	10	2	B39308	glycine reductase
3	15	38.5	11	4	I52708	ELAV-like neuronal
4	15	38.5	12	2	PT0228	Ig heavy chain CDR
5	15	38.5	12	2	PC4377	telomeric and tetr
6	14	35.9	7	2	PT0246	Ig heavy chain CRD
7	14	35.9	9	2	S78420	ribosomal protein
8	14	35.9	10	2	B56899	serum heterodimer,
9	14	35.9	11	2	PQ0733	unidentified 6.0/1
10	14	35.9	12	2	S09082	proteasome chain 1
11	13	33.3	6	2	S02617	alcohol dehydrogen
12	13	33.3	6	2	B56979	collagen alpha 1(I
13	13	33.3	7	2	PT0520	T-cell receptor be
14	13	33.3	8	2	S65381	cytochrome-c oxida
15	13	33.3	8	2	S69165	ferredoxin a2 - Ja
16	13	33.3	9	2	T31612	hypothetical prote
17	13	33.3	9	2	A42266	peptidylglycine mo
18	13	33.3	9	2	A60427	macrophage cytotox
19	13	33.3	9	2	S39437	D-amino-acid oxida
20	13	33.3	10	2	S13224	virG protein - Agr
21	13	33.3	10	2	T14212	cytochrome-c oxida
22	13	33.3	10	2	S23307	neurokinin A - rai
23	13	33.3	10	2	S23186	neurokinin A - Atl
24	13	33.3	11	2	S23364	T-cell receptor al
25	13	33.3	12	2	C30503	Ig gamma-2b chain
26	12	30.8	7	2	I46868	alpha-myosin heavy
27	12	30.8	9	2	B45796	dihydrolipoamide S
28	12	30.8	9	2	A61102	parathyroid hormon
29	12	30.8	9	2	PS0253	glycine cleavage s
30	12	30.8	9	2	A56029	N-methylpurine DNA
31	12	30.8	10	2	JN0440	peptide-N4-(N-acet
32	12	30.8	10	2	S77980	cytochrome-c oxida
33	12	30.8	10	2	A30823	bothropstoxin - ja
34	12	30.8	11	2	H54346	pyruvate synthase
35	12	30.8	11	2	S78765	ribosomal protein
36	12	30.8	12	2	C34135	DNA-binding protei
37	12	30.8	12	2	S65730	hemoglobin, extrac
38	12	30.8	12	2	S21163	NAD ADP-ribosyltra
39	12	30.8	12	2	PQ0730	unidentified 5.4/3
40	11	28.2	6	2	S11024	hydrogensulfite re
41	11	28.2	6	2	B44510	hypothetical prote
42	11	28.2	7	2	S57274	triacylglycerol li
43	11	28.2	8	2	PT0298	Ig heavy chain CRD
44	11	28.2	8	2	A35768	T-cell receptor al
45	11	28.2	9	2	I54379	gene NF2 protein -

ALIGNMENTS

RESULT 1
PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C;Accession: PC4374
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4374
A;Molecule type: protein
A;Residues: 1-10 <SAR>
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 46.2%; Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 KXHRV 5
              | ||:
Db          6 KEHRL 10
```

RESULT 2
B39308
glycine reductase (EC 1.4.99.-) sulfhydryl protein C, beta chain - Clostridium sticklandi
C;Species: Clostridium sticklandii
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C;Accession: B39308
R;Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A;Title: Glycine reductase protein C. Properties and characterization of its role in the
A;Reference number: A39308; MUID:92042141; PMID:1939235
A;Accession: B39308
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <STA>
A;Cross-references: UNIPROT:Q9EV92
C;Function:
A;Description: glycine reductase complex catalyzes the reductive deamination of glycine t
C;Keywords: ATP; oxidoreductase

Query Match 41.0%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 HRVIKD 8
              ::|| |
Db          4 NKVIAD 9
```

```
RESULT 3
I52708
ELAV-like neuronal protein 1, truncated splice form - human
N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: I52708
R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis
A;Reference number: I52708; MUID:94349312; PMID:8069866
A;Accession: I52708
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-11 <SEK>
A;Cross-references: UNIPROT:Q16234; GB:S73887; NID:g688242; PIDN:AAD14142.1; PID:g426184
C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
C;Genetics:
A;Gene: GDB:ELAVL4; HUD; PNEM
A;Cross-references: GDB:141875; OMIM:168360
A;Map position: 1p36-1p36
C;Keywords: alternative splicing

  Query Match             38.5%;  Score 15;  DB 4;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 4.5e+03;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 RVIK 7
              |::|
Db          6 RILK 9


RESULT 4
PT0228
Ig heavy chain CDR3 region (clone 1-112) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0228
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0228
A;Molecule type: DNA
A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             38.5%;  Score 15;  DB 2;  Length 12;
  Best Local Similarity   40.0%;  Pred. No. 4.9e+03;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 RVIKD 8
              | ::|
Db          2 RYVRD 6


RESULT 5
PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: PC4377
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4377
A;Molecule type: protein
A;Residues: 1-12 <SAR>
A;Cross-references: UNIPROT:Q9QX80; UNIPROT:Q9Z0U8; UNIPROT:O88311; UNIPROT:Q9QX81
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

  Query Match             38.5%;  Score 15;  DB 2;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 4.9e+03;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRV 5
              | | |
Db          3 KFHTV 7


RESULT 6
PT0246
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0246
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0246
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             35.9%;  Score 14;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVI 6
              | |:
Db          1 HEVL 4


RESULT 7
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

  Query Match             35.9%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRV 5
              ||:
Db          5 HRL 7


RESULT 8
B56899
serum heterodimer, 24K chain - sandbar shark (fragment)
C;Species: Carcharhinus plumbeus (sandbar shark)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: B56899
R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by
A;Reference number: A56899; MUID:93092592; PMID:1458832
A;Accession: B56899
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAZ>
A;Cross-references: UNIPROT:Q7LZJ7
```

```
C;Keywords: glycoprotein; plasma

  Query Match             35.9%;  Score 14;  DB 2;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 6.7e+03;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 RVIKD 8
              ||: :
Db          6 RVVNE 10


RESULT 9
PQ0733
unidentified 6.0/15K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0733
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696
A;Accession: PQ0733
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <KOM>

  Query Match             35.9%;  Score 14;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 7.4e+03;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVI 6
              | :|
Db          1 HTII 4


RESULT 10
S09082
proteasome chain 1 - rat (fragment)
N;Alternate names: multicatalytic proteinase chain 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09082
R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.
FEBS Lett. 262, 327-329, 1990
A;Title: N-terminal sequence similarities between components of the multicatalytic prote
A;Reference number: S09082; MUID:90242957; PMID:2335214
A;Accession: S09082
A;Molecule type: protein
A;Residues: 1-12 <LIL>
C;Superfamily: multicatalytic endopeptidase complex chain C9

  Query Match             35.9%;  Score 14;  DB 2;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 8e+03;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 VIKD 8
              | ||
Db          7 VYKD 10


RESULT 11
S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S02617
R;Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall
FEBS Lett. 222, 99-103, 1987
A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differenc
A;Reference number: S02617; MUID:88005160; PMID:3653405
A;Accession: S02617
A;Molecule type: protein
A;Residues: 1-6 <FAI>
A;Cross-references: UNIPROT:P19854
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

  Query Match             33.3%;  Score 13;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 VIK 7
              |||
Db          4 VIK 6


RESULT 12
B56979
collagen alpha 1(II) chain - bovine (fragment)
N;Alternate names: collagen alpha 3(XI) chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C;Accession: B56979
R;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Insi
A;Reference number: A56978; MUID:95370194; PMID:7642541
A;Accession: B56979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <WUA>
A;Note: the residue designated "X" is modified Lysine in collagen 1(II) some cross-linkec

  Query Match             33.3%;  Score 13;  DB 2;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HR 4
              ||
Db          5 HR 6


RESULT 13
PT0520
T-cell receptor beta chain V-D-J region (100-4F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0520
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0520
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             33.3%;  Score 13;  DB 2;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KXH 3
              | |
Db          5 KAH 7


RESULT 14
S65381
cytochrome-c oxidase (EC 1.9.3.1) chain VIb, hepatic - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65381
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
```

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65381
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <SCH>
A;Cross-references: UNIPROT:P80430
C;Keywords: oxidoreductase

Query Match 33.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HR 4
||
Db 7 HR 8

RESULT 15
S69165
ferredoxin a2 - Japanese radish (fragment)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 09-Jul-2004
C;Accession: S69165
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69165
A;Molecule type: protein
A;Residues: 1-8 <OBA>
A;Cross-references: UNIPROT:Q7M1F1
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 33.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HR 4
||
Db 2 HR 3

Search completed: October 21, 2004, 07:27:57
Job time : 17.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIKDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	92.3	9	15	US-10-447-161-84	Sequence 84, Appl
2	36	92.3	9	16	US-10-788-016-1	Sequence 1, Appli
3	28	71.8	9	9	US-09-984-056-61	Sequence 61, Appl
4	28	71.8	9	9	US-09-984-056-62	Sequence 62, Appl
5	28	71.8	9	9	US-09-984-057-61	Sequence 61, Appl
6	28	71.8	9	9	US-09-984-057-62	Sequence 62, Appl
7	28	71.8	9	14	US-10-105-232-61	Sequence 61, Appl
8	28	71.8	9	14	US-10-105-232-62	Sequence 62, Appl
9	28	71.8	9	14	US-10-189-437-61	Sequence 61, Appl
10	28	71.8	9	14	US-10-189-437-62	Sequence 62, Appl
11	24	61.5	9	14	US-10-211-207-23	Sequence 23, Appl
12	24	61.5	9	14	US-10-211-207-24	Sequence 24, Appl
13	24	61.5	9	14	US-10-077-106-23	Sequence 23, Appl
14	24	61.5	9	14	US-10-077-106-24	Sequence 24, Appl
15	23	59.0	10	9	US-09-851-138-204	Sequence 204, App
16	23	59.0	11	9	US-09-984-056-72	Sequence 72, Appl
17	23	59.0	11	9	US-09-984-057-72	Sequence 72, Appl
18	23	59.0	11	14	US-10-105-232-72	Sequence 72, Appl
19	23	59.0	11	14	US-10-189-437-72	Sequence 72, Appl
20	22	56.4	10	10	US-09-876-904A-145	Sequence 145, App
21	22	56.4	11	14	US-10-293-822-14	Sequence 14, Appl
22	22	56.4	11	14	US-10-293-822-22	Sequence 22, Appl
23	22	56.4	12	14	US-10-300-575-4	Sequence 4, Appli
24	22	56.4	12	15	US-10-601-953-76	Sequence 76, Appl
25	21	53.8	9	14	US-10-119-536A-14	Sequence 14, Appl
26	21	53.8	10	10	US-09-876-904A-500	Sequence 500, App
27	21	53.8	10	10	US-09-833-039-114	Sequence 114, App
28	21	53.8	10	14	US-10-124-903-12	Sequence 12, Appl
29	21	53.8	10	14	US-10-177-277-114	Sequence 114, App
30	21	53.8	12	10	US-09-876-904A-173	Sequence 173, App
31	20.5	52.6	11	10	US-09-876-904A-578	Sequence 578, App
32	20	51.3	7	14	US-10-369-226-26	Sequence 26, Appl
33	20	51.3	7	17	US-10-459-030B-65	Sequence 65, Appl
34	20	51.3	8	9	US-09-984-056-54	Sequence 54, Appl
35	20	51.3	8	9	US-09-234-395-314	Sequence 314, App
36	20	51.3	8	9	US-09-305-928-314	Sequence 314, App
37	20	51.3	8	9	US-09-984-057-54	Sequence 54, Appl
38	20	51.3	8	9	US-09-769-145-48	Sequence 48, Appl
39	20	51.3	8	13	US-10-006-982-46	Sequence 46, Appl
40	20	51.3	8	14	US-10-105-008-48	Sequence 48, Appl
41	20	51.3	8	14	US-10-058-821-30	Sequence 30, Appl
42	20	51.3	8	14	US-10-105-232-54	Sequence 54, Appl
43	20	51.3	8	14	US-10-189-437-54	Sequence 54, Appl
44	20	51.3	8	14	US-10-359-546-60	Sequence 60, Appl
45	20	51.3	8	15	US-10-425-557-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 92.3%; Score 36; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 KXHRVIKD 8
              | ||||||
Db          1 KFHRVIKD 8
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RESULT 2
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo

; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophillin B
US-10-788-016-1

Query Match 92.3%; Score 36; DB 16; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| ||||||
Db 1 KFHRVIKD 8

RESULT 3
US-09-984-056-61
; Sequence 61, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-61

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| || :||
Db 1 KQHRELKD 8

RESULT 4
US-09-984-056-62
; Sequence 62, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-62

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| || :||
Db 1 KQHRELKD 8

RESULT 5
US-09-984-057-61
; Sequence 61, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-057-61

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| || :||
Db 1 KQHRELKD 8

RESULT 6
US-09-984-057-62
; Sequence 62, Application US/09984057

```
; Patent No. US20020151677A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING
;  TITLE OF INVENTION:  REPLIKIN-CONTAINING SEQUENCES
;  FILE REFERENCE: 09425-46902
;  CURRENT APPLICATION NUMBER: US/09/984,057
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-09-984-057-62

  Query Match             71.8%;  Score 28;  DB 9;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 7
US-10-105-232-61
; Sequence 61, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
;  TITLE OF INVENTION:  AND IN INFLUENZA EPIDEMICS
;  FILE REFERENCE: 09425-46904
;  CURRENT APPLICATION NUMBER: US/10/105,232
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-10-105-232-61

  Query Match             71.8%;  Score 28;  DB 14;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 8
US-10-105-232-62
; Sequence 62, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
;  TITLE OF INVENTION:  AND IN INFLUENZA EPIDEMICS
;  FILE REFERENCE: 09425-46904
;  CURRENT APPLICATION NUMBER: US/10/105,232
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-10-105-232-62

  Query Match             71.8%;  Score 28;  DB 14;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 9
US-10-189-437-61
; Sequence 61, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
;  FILE REFERENCE: 09425/46905
;  CURRENT APPLICATION NUMBER: US/10/189,437
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: 10/105,232
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: 09/984,057
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 729
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-10-189-437-61

  Query Match             71.8%;  Score 28;  DB 14;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
```

```
              | || :||
Db          1 KQHRELKD 8


RESULT 10
US-10-189-437-62
; Sequence 62, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
;  FILE REFERENCE: 09425/46905
;  CURRENT APPLICATION NUMBER: US/10/189,437
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: 10/105,232
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: 09/984,057
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 729
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-10-189-437-62

  Query Match             71.8%;  Score 28;  DB 14;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIKD 8
              | || :||
Db          1 KQHRELKD 8


RESULT 11
US-10-211-207-23
; Sequence 23, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
;  APPLICANT: Collins, Mary
;  APPLICANT:  Madrenas, Joaquin
;  APPLICANT:  Carreno, Beatriz
;  APPLICANT:  Kuchroo, Vijay
;  TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
;  TITLE OF INVENTION:  RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
;  TITLE OF INVENTION:  PP2A
;  FILE REFERENCE: GNN-027
;  CURRENT APPLICATION NUMBER: US/10/211,207
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US/10/077,106
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyomavirus small
US-10-211-207-23

  Query Match             61.5%;  Score 24;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              || :||
Db          1 HRELKD 6


RESULT 12
US-10-211-207-24
; Sequence 24, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
;  APPLICANT: Collins, Mary
;  APPLICANT:  Madrenas, Joaquin
;  APPLICANT:  Carreno, Beatriz
;  APPLICANT:  Kuchroo, Vijay
;  TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
;  TITLE OF INVENTION:  RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
;  TITLE OF INVENTION:  PP2A
;  FILE REFERENCE: GNN-027
;  CURRENT APPLICATION NUMBER: US/10/211,207
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US/10/077,106
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyomavirus medium
US-10-211-207-24

  Query Match             61.5%;  Score 24;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              || :||
Db          1 HRELKD 6


RESULT 13
US-10-077-106-23
; Sequence 23, Application US/10077106
; Publication No. US20030166531A1
; GENERAL INFORMATION:
;  APPLICANT: Collins, Mary
;  APPLICANT:  Madrenas, Joaquin
;  APPLICANT:  Carreno, Beatriz
;  APPLICANT:  Kuchroo, Vijay
;  TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
;  TITLE OF INVENTION:  RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
;  TITLE OF INVENTION:  PP2A
;  FILE REFERENCE: GNN-027
;  CURRENT APPLICATION NUMBER: US/10/077,106
;  CURRENT FILING DATE:  2002-02-15
;  PRIOR APPLICATION NUMBER: 60/269,757
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyomavirus small
US-10-077-106-23

  Query Match             61.5%;  Score 24;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              || :||
Db          1 HRELKD 6


RESULT 14
US-10-077-106-24
; Sequence 24, Application US/10077106
; Publication No. US20030166531A1
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; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/077,106
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,757
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyomavirus medium
US-10-077-106-24

Query Match 61.5%; Score 24; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 HRVIKD 8
              || :||
Db          1 HRELKD 6
```

RESULT 15
US-09-851-138-204
; Sequence 204, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204

Query Match 59.0%; Score 23; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KXHRVIKD 8
              | |:| :|
Db          3 KYHQVTQD 10
```

Search completed: October 21, 2004, 07:33:41
Job time : 62.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIKDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	53.8	8	2	Q8AWV7	Q8awv7 anas platyr
2	21	53.8	8	2	Q8AWV8	Q8awv8 cygnus colu
3	21	53.8	8	2	Q8AWV9	Q8awv9 anser caeru
4	21	53.8	8	2	Q8AWW0	Q8aww0 coscoroba c
5	20	51.3	8	2	Q05403	Q05403 saccharomyc
6	19	48.7	9	2	Q7SCD2	Q7scd2 neurospora
7	19	48.7	10	2	Q8N6B1	Q8n6b1 homo sapien
8	19	48.7	10	2	Q8RJF1	Q8rjf1 pseudomonas
9	19	48.7	11	2	Q9XSP2	Q9xsp2 hylobates s
10	19	48.7	11	2	Q9XSP5	Q9xsp5 pan troglod
11	19	48.7	11	2	Q9XSP6	Q9xsp6 pongo pygma
12	19	48.7	11	2	Q9XSP7	Q9xsp7 pygathrix n
13	19	48.7	11	2	Q9XSP8	Q9xsp8 presbytis j
14	19	48.7	11	2	Q9XSQ4	Q9xsq4 gorilla gor
15	18	46.2	12	2	Q7RGL4	Q7rgl4 plasmodium
16	17	43.6	9	2	Q9TWX7	Q9twx7 manduca sex
17	17	43.6	10	2	Q9TQV4	Q9tqv4 e equus cab
18	17	43.6	11	2	Q8MEL7	Q8mel7 sida hooker
19	17	43.6	11	2	Q8MEL9	Q8mel9 pavonia has
20	17	43.6	11	2	Q8MEM2	Q8mem2 lagunaria p
21	17	43.6	11	2	Q8MEP0	Q8mep0 hibiscus pe
22	17	43.6	11	2	Q8MEP3	Q8mep3 hibiscus no
23	17	43.6	11	2	Q8MEP5	Q8mep5 hibiscus mi
24	17	43.6	11	2	Q8MEQ7	Q8meq7 hibiscus dr
25	17	43.6	11	2	Q8MER0	Q8mer0 hibiscus co
26	17	43.6	11	2	Q8MER1	Q8mer1 hibiscus ca
27	17	43.6	11	2	Q8MER7	Q8mer7 fioria viti
28	17	43.6	11	2	Q8MER8	Q8mer8 dombeya til
29	17	43.6	11	2	Q8MES1	Q8mes1 alyogyne pi
30	17	43.6	11	2	Q8MES3	Q8mes3 alyogyne cr
31	17	43.6	11	2	Q8MES5	Q8mes5 abelmoschus
32	17	43.6	12	2	Q8HU93	Q8hu93 bryum donia
33	17	43.6	12	2	Q8LU67	Q8lu67 macrostelia
34	17	43.6	12	2	Q8MEL6	Q8mel6 thespesia t
35	17	43.6	12	2	Q8MEL8	Q8mel8 radyera far
36	17	43.6	12	2	Q8MEM0	Q8mem0 malvaviscus
37	17	43.6	12	2	Q8MEM1	Q8mem1 malva negle
38	17	43.6	12	2	Q8MEM4	Q8mem4 hibiscus zo
39	17	43.6	12	2	Q8MEM5	Q8mem5 hibiscus wa
40	17	43.6	12	2	Q8MEM6	Q8mem6 hibiscus tr
41	17	43.6	12	2	Q8MEM7	Q8mem7 hibiscus ti
42	17	43.6	12	2	Q8MEM8	Q8mem8 hibiscus sy
43	17	43.6	12	2	Q8MEM9	Q8mem9 hibiscus su
44	17	43.6	12	2	Q8MEN0	Q8men0 hibiscus st
45	17	43.6	12	2	Q8MEN1	Q8men1 hibiscus st

ALIGNMENTS

RESULT 1
Q8AWV7
ID Q8AWV7 PRELIMINARY; PRT; 8 AA.
AC Q8AWV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY123327; AAM96901.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 53.8%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7
```

RESULT 2
Q8AWV8
ID Q8AWV8 PRELIMINARY; PRT; 8 AA.
AC Q8AWV8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Cygnus columbianus (tundra swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
OX NCBI_TaxID=110926;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY123326; AAM96900.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 53.8%; Score 21; DB 2; Length 8;

```
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 3
Q8AWV9
ID   Q8AWV9      PRELIMINARY;      PRT;     8 AA.
AC   Q8AWV9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Anser caerulescens caerulescens (snow goose).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX   NCBI_TaxID=70340;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123325; AAM96899.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             53.8%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 4
Q8AWW0
ID   Q8AWW0      PRELIMINARY;      PRT;     8 AA.
AC   Q8AWW0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Coscoroba coscoroba (Coscoroba swan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
OX   NCBI_TaxID=8863;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123324; AAM96898.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             53.8%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 5
Q05403
ID   Q05403      PRELIMINARY;      PRT;     8 AA.
AC   Q05403;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Orf 00915 protein (Fragment).
GN   Name=orf 00915;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FY1679;
RX   MEDLINE=96021609; PubMed=8533473;
RA   Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT   "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT   more than twice as many unknown open reading frames.";
RL   Yeast 11:975-986(1995).
DR   EMBL; X83121; CAA58183.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  879 MW;  7B5322D2C441E058 CRC64;

  Query Match             51.3%;  Score 20;  DB 2;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              | |:|
Db          3 HNVVK 7


RESULT 6
Q7SCD2
ID   Q7SCD2      PRELIMINARY;      PRT;     9 AA.
AC   Q7SCD2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Predicted protein.
GN   Name=NCU05334.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000130; EAA34319.1; -.
SQ   SEQUENCE   9 AA;  1173 MW;  C483A32B50440449 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          3 HRVIKD 8
              :|: ||
Db          3 NRIYKD 8


RESULT 7
Q8N6B1
ID   Q8N6B1      PRELIMINARY;      PRT;    10 AA.
AC   Q8N6B1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Capacitative calcium channel protein Trp1 (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Late pregnancy myometrium;
RX   MEDLINE=22181008; PubMed=12193412;
RA   Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,
RA   Sanborn B.M.;
RT   "Multiple Trp isoforms implicated in capacitative calcium entry are
RT   expressed in human pregnant myometrium and myometrial cells.";
RL   Biol. Reprod. 67:988-994(2002).
DR   EMBL; AF483646; AAM97861.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1336 MW;  0DD0C0B401F40724 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || ||
Db          6 HRDIK 10


RESULT 8
Q8RJF1
ID   Q8RJF1      PRELIMINARY;      PRT;    10 AA.
AC   Q8RJF1;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Porin-like protein (Fragment).
OS   Pseudomonas fluorescens.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=294;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NC16-2, TC29-5, and TC97;
RX   MEDLINE=22315381; PubMed=12427948;
RA   Kholodii G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;
RT   "Tn5041-like transposons: molecular diversity, evolutionary
RT   relationships and distribution of distinct variants in environmental
RT   bacteria.";
RL   Microbiology 148:3569-3582(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NC16-2, TC29-5, and TC97;
RA   Kholodii G.Y.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ422128; CAD19527.1; -.
DR   EMBL; AJ422129; CAD19528.1; -.
DR   EMBL; AJ422130; CAD19529.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005741; C:mitochondrial outer membrane; IEA.
DR   GO; GO:0015288; F:porin activity; IEA.
KW   Porin.
FT   NON_TER *     10     10
SQ   SEQUENCE   10 AA;  1206 MW;  23C47E7401F5A417 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 2.9e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KXHRVIK 7
              : || |:
Db          4 RSHRPIR 10


RESULT 9
Q9XSP2
ID   Q9XSP2      PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9590;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243280; CAB45927.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || :|
Db          7 HRSVK 11


RESULT 10
Q9XSP5
ID   Q9XSP5      PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243277; CAB45926.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1331 MW;  7FB881F101E1F2D4 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
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```
          || :|
Db          7 HRSVK 11


RESULT 11
Q9XSP6
ID   Q9XSP6       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243279; CAB45925.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || :|
Db          7 HRSVK 11


RESULT 12
Q9XSP7
ID   Q9XSP7       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pygathrix nemaeus (Dove langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=54133;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243282; CAB45924.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || :|
Db          7 HRSVK 11


RESULT 13
Q9XSP8
ID   Q9XSP8       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Presbytis johnii.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Presbytis.
OX   NCBI_TaxID=98375;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243281; CAB46013.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || :|
Db          7 HRSVK 11


RESULT 14
Q9XSQ4
ID   Q9XSQ4       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSQ4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243278; CAB45916.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1331 MW;  7FB881F101E1F2D4 CRC64;

  Query Match             48.7%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              || :|
Db          7 HRSVK 11


RESULT 15
Q7RGL4
ID   Q7RGL4       PRELIMINARY;      PRT;    12 AA.
AC   Q7RGL4;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein (Fragment).
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```
GN   Name=PY04332;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=17XNL;
RX   PubMed=12368865;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01001307; EAA16180.1; -.
KW   Hypothetical protein.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1485 MW;  D2A760BC2E633DC2 CRC64;

  Query Match             46.2%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 5.8e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              |:| |
Db          3 HKVAK 7

Search completed: October 21, 2004, 07:26:47
Job time : 87 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	92.5	9	3	AAY69963	Aay69963 Human cyc
2	37	92.5	9	3	AAY69958	Aay69958 Human cyc
3	37	92.5	9	3	AAY69961	Aay69961 Human cyc
4	37	92.5	9	3	AAY69922	Aay69922 Human cyc
5	37	92.5	9	4	AAB46947	Aab46947 Human cyc
6	37	92.5	9	4	AAB46931	Aab46931 Human cyc
7	37	92.5	9	4	AAG68089	Aag68089 Antitumou
8	37	92.5	9	5	ABG79076	Abg79076 Human Cyp
9	37	92.5	9	6	ABR84374	Abr84374 Human Cyp
10	37	92.5	9	7	ADC17709	Adc17709 Modified
11	37	92.5	9	7	ADC17702	Adc17702 Cyclophil
12	37	92.5	9	8	ADG89642	Adg89642 Class I H
13	27	67.5	9	3	AAY69957	Aay69957 Human cyc
14	25	62.5	8	3	AAB12089	Aab12089 Ad7 ce1 p
15	25	62.5	8	7	ADE84662	Ade84662 Adenoviru
16	25	62.5	9	2	AAR20729	Aar20729 Pancreas-
17	25	62.5	9	3	AAY51905	Aay51905 Elastase
18	25	62.5	10	5	AAU78392	Aau78392 Biosurfac
19	24	60.0	9	8	ADK07318	Adk07318 Hepatitis
20	24	60.0	9	8	ADK06815	Adk06815 Hepatitis
21	23	57.5	6	2	AAW83889	Aaw83889 Peptide s
22	23	57.5	11	2	AAW48850	Aaw48850 Human pro
23	22	55.0	9	4	AAB45861	Aab45861 Human tum
24	22	55.0	10	6	ABR83253	Abr83253 H. pylori
25	22	55.0	11	8	ADN17045	Adn17045 Gi-alpha
26	22	55.0	12	6	ABR01459	Abr01459 Human TIM
27	22	55.0	12	7	ABR63060	Abr63060 Pathogen
28	21	52.5	5	6	AAE34120	Aae34120 Gluten sp
29	21	52.5	8	2	AAR93207	Aar93207 New contr
30	21	52.5	9	2	AAR72938	Aar72938 E. coli P
31	21	52.5	9	2	AAR72894	Aar72894 E. coli P
32	21	52.5	9	6	ABR67369	Abr67369 Human hsp
33	21	52.5	9	6	ABR67364	Abr67364 Human hsp
34	21	52.5	9	8	ADK07060	Adk07060 Hepatitis
35	21	52.5	10	2	AAR72949	Aar72949 E. coli P
36	21	52.5	10	2	AAR72905	Aar72905 E. coli P
37	21	52.5	10	2	AAW41471	Aaw41471 Fragment
38	21	52.5	10	3	AAB35991	Aab35991 Sorbitol
39	21	52.5	10	4	AAG87272	Aag87272 Saccharom
40	21	52.5	10	7	ADI15749	Adi15749 HLA-A2 re
41	21	52.5	10	8	ADJ52136	Adj52136 CH1 delet
42	21	52.5	10	8	ADK09152	Adk09152 Human pap
43	21	52.5	10	8	ADK09635	Adk09635 Human pap
44	21	52.5	10	8	ADO17328	Ado17328 Different
45	21	52.5	11	2	AAR14821	Aar14821 Bay thioe

ALIGNMENTS

RESULT 1
AAY69963
ID AAY69963 standard; peptide; 9 AA.
XX
AC AAY69963;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #43.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||

```
Db          1 DYMIQGGD 8


RESULT 2
AAY69958
ID   AAY69958 standard; peptide; 9 AA.
XX
AC   AAY69958;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #38.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 61; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             92.5%;  Score 37;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DFMIQGGD 8


RESULT 3
AAY69961
ID   AAY69961 standard; peptide; 9 AA.
XX
AC   AAY69961;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #41.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Tyr, Met, Trp
FT   Misc-difference 9
FT                   /label= Phe, Leu, Ile, Trp, Met
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 10; Page 60; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             92.5%;  Score 37;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              ||||||||
Db          1 DXMIQGGD 8


RESULT 4
AAY69922
ID   AAY69922 standard; peptide; 9 AA.
XX
AC   AAY69922;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #2.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 49; 64pp; Japanese.
XX
```

CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DFMIQGGD 8

RESULT 5
AAB46947
ID AAB46947 standard; peptide; 9 AA.
XX
AC AAB46947;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 20; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DYMIQGGD 8

RESULT 6
AAB46931
ID AAB46931 standard; peptide; 9 AA.
XX
AC AAB46931;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 15; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DFMIQGGD 8

RESULT 7
AAG68089
ID AAG68089 standard; peptide; 9 AA.
XX

AC AAG68089;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 91-99.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DFMIQGGD 8

RESULT 8
ABG79076
ID ABG79076 standard; peptide; 9 AA.
XX
AC ABG79076;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #2.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DFMIQGGD 8

RESULT 9
ABR84374
ID ABR84374 standard; peptide; 9 AA.
XX
AC ABR84374;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:24.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX

OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DFMIQGGD 8

RESULT 10
ADC17709
ID ADC17709 standard; peptide; 9 AA.
XX
AC ADC17709;
XX
DT 18-DEC-2003 (first entry)
XX
DE Modified cyclophilin B protein amino acids 91-99.
XX
KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX
PN WO2003020306-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002WO-JP008641.
XX
PR 29-AUG-2001; 2001JP-00260046.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Yamada A;
XX
DR WPI; 2003-300831/29.
XX
PT Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 9; 49pp; Japanese.
XX
CC The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet dos not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 91-99 of the cyclophilin B protein with the
CC Phe at position 92 replaced by a Tyr.
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 7; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| ||||||
Db 1 DYMIQGGD 8

RESULT 11
ADC17702
ID ADC17702 standard; peptide; 9 AA.
XX
AC ADC17702;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cyclophilin B protein amino acids 91-99.
XX
KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX
PN WO2003020306-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002WO-JP008641.
XX
PR 29-AUG-2001; 2001JP-00260046.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Yamada A;
XX
DR WPI; 2003-300831/29.
XX
PT Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 2; 49pp; Japanese.
XX
CC The invention relates to allergic reaction suppressors, comprising a

```
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 91-99 of the cyclophilin B protein.
XX
SQ   Sequence 9 AA;

  Query Match             92.5%;  Score 37;  DB 7;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DFMIQGGD 8


RESULT 12
ADG89642
ID   ADG89642 standard; peptide; 9 AA.
XX
AC   ADG89642;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Class I HLA-restricted widely expressed antigen #7.
XX
KW   metastatic cancer cell differentiation; mutated fibronectin;
KW   metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS   Unidentified.
XX
PN   WO2003100027-A2.
XX
PD   04-DEC-2003.
XX
PF   28-MAY-2003; 2003WO-US016736.
XX
PR   28-MAY-2002; 2002US-0383530P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Wang R;
XX
DR   WPI; 2004-035134/03.
XX
PT   Identifying a cell that differentiates into a metastatic cancer cell,
PT   useful for preventing metastatic cancer, comprises identifying a mutated
PT   fibronectin in the cell.
XX
PS   Disclosure; SEQ ID NO 85; 137pp; English.
XX
CC   The invention comprises a method for identifying a cell that will
CC   differentiate into a metastatic cancer cell, the method involves
CC   identifying a mutated fibronectin in the cell. The method of the
CC   invention is useful for preventing metastatic cancer. The present amino
CC   acid sequence represents a Class I HLA-restricted widely expressed
CC   antigen.
XX
SQ   Sequence 9 AA;

  Query Match             92.5%;  Score 37;  DB 8;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DFMIQGGD 8


RESULT 13
AAY69957
ID   AAY69957 standard; peptide; 9 AA.
XX
AC   AAY69957;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #37.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 61; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             67.5%;  Score 27;  DB 3;  Length 9;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              | ||||
Db          3 MCQGGD 8


RESULT 14
AAB12089
ID   AAB12089 standard; peptide; 8 AA.
XX
AC   AAB12089;
XX
DT   12-SEP-2003  (revised)
DT   17-JAN-2001  (first entry)
XX
DE   Ad7 cel peptide.
XX
KW   Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;
KW   cell proliferation; cell differentiation; tissue repair;
KW   transcription regulator; breast cancer; gene therapy; melanoma;
KW   neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease;
KW   Alzheimer's disease; paralysis; motor neurone disorder; cel.
XX
OS   unidentified adenovirus.
XX
```

PN US6069231-A.
XX
PD 30-MAY-2000.
XX
PF 18-AUG-1995; 95US-00516859.
XX
PR 18-AUG-1994; 94US-00292683.
PR 06-MAR-1995; 95US-00399411.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Huang S;
XX
DR WPI; 2000-410879/35.
XX
PT New PR domain peptides comprising amino acid sequences from, for example
PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for
PT regulating gene transcription and controlling cell proliferation and
PT differentiation.
XX
PS Disclosure; Fig 2; 91pp; English.
XX
CC The present sequence is Ad7 ce1 from Adenovirus. The ce1 domain is also
CC found in rat retinoblastoma (Rb)-interacting zinc finger (RIZ) protein
CC (AAB12028). RIZ is a nuclear phosphoprotein that acts as a cell
CC differentiation factor. RIZ can modulate cell growth by binding to Rb
CC protein, which is involved in regulating cell proliferation. In addition,
CC RIZ can act to regulate transcription. RIZ functions to maintain cells in
CC the G1 phase of the cell cycle, by interacting with Rb through the cr2
CC domain of RIZ. Rat RIZ protein contains a number of GTPase motifs (see
CC AAB12037 to AAB12056 and AAB12099 to AAB12104). RIZ protein is a PR
CC domain protein and is present primarily in the cell nucleus. RIZ gene
CC mutations may be implicated in various cancers such as melanoma,
CC neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be
CC used in gene therapy for these disorders. Since RIZ protein is implicated
CC in cell cycle arrest, inhibition of RIZ activity may be useful in
CC neurodegenerative disorder therapy e.g. for Parkinson's, Huntingdon's or
CC Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
CC disorders e.g. heart disease, where the ability to induce neural/ cardiac
CC tissue proliferation would be useful. The present sequence was used for
CC sequence homology comparison. (Updated on 12-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 8 AA;

Query Match 62.5%; Score 25; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
: :::|||
Db 1 EDLLEGGD 8

RESULT 15
ADE84662
ID ADE84662 standard; peptide; 8 AA.
XX
AC ADE84662;
XX
DT 29-JAN-2004 (first entry)
XX
DE Adenovirus 7 E1A gene ce1 domain.
XX
KW cytostatic; tumor; gene therapy;
KW retinoblastoma protein-interacting zinc protein; RIZ; neuroblastoma;
KW melanoma; cardiac cell growth inducer; neuronal cell growth inducer;
KW adenovirus; E1A; ce1.
XX
OS unidentified adenovirus.
XX
PN US6468985-B1.
XX
PD 22-OCT-2002.
XX
PF 17-MAR-2000; 2000US-00528706.
XX
PR 18-AUG-1994; 94US-00292683.
PR 06-MAR-1995; 95US-00399411.
PR 18-AUG-1995; 95US-00516859.
XX
PA (BURN-) BURNHAM INST.
XX
PI Huang S;
XX
DR WPI; 2003-147106/14.
XX
PT Reducing the growth of tumor cell having mammalian retinoblastoma protein
PT -interacting zinc finger proteins in a subject, comprises administering
PT nucleic acid molecule encoding RIZ at or adjacent to the site of tumor.
XX
PS Example 3; SEQ ID NO 75; 49pp; English.
XX
CC The invention describes a method of reducing growth of a tumour cell
CC having a mutant mammalian retinoblastoma (Rb) protein-interacting zinc
CC finger (RIZ) protein in a subject The method comprises administering a
CC nucleic acid molecule (I) encoding RIZ at or adjacent to tumour site. (I)
CC is administered at the site of the tumour. The method is useful for
CC reducing the growth of a tumour cell e.g. neuroblastoma or melanoma cell
CC having mutant RIZ protein. The method is useful for inducing growth of a
CC cardiac cell or a neuronal cell in a subject, and for effecting normal
CC growth control to a tumour cell or causing differentiation of tumour
CC cells. This is the amino acid sequence of an adenovirus cr1 domain used
CC in a comparison with the ce1 domain of RIZ protein.
XX
SQ Sequence 8 AA;

Query Match 62.5%; Score 25; DB 7; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
: :::|||
Db 1 EDLLEGGD 8

Search completed: October 21, 2004, 07:21:01
Job time : 86 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	62.5	8	2	US-08-459-568-75	Sequence 75, Appl
2	25	62.5	8	2	US-08-399-411-75	Sequence 75, Appl
3	25	62.5	8	3	US-08-516-859A-75	Sequence 75, Appl
4	25	62.5	8	3	US-09-586-472-75	Sequence 75, Appl
5	25	62.5	8	4	US-09-528-706-75	Sequence 75, Appl
6	25	62.5	9	1	US-08-457-172-1	Sequence 1, Appli
7	23	57.5	8	1	US-08-487-860-62	Sequence 62, Appl
8	23	57.5	11	3	US-08-953-327-1	Sequence 1, Appli
9	23	57.5	11	3	US-09-472-579-1	Sequence 1, Appli
10	22	55.0	9	1	US-08-215-805A-7	Sequence 7, Appli
11	22	55.0	9	1	US-08-215-805A-52	Sequence 52, Appl
12	22	55.0	9	1	US-08-215-805A-58	Sequence 58, Appl
13	21	52.5	10	3	US-09-296-284-10	Sequence 10, Appl
14	21	52.5	11	1	US-07-620-426B-19	Sequence 19, Appl
15	21	52.5	11	1	US-07-662-007B-19	Sequence 19, Appl
16	21	52.5	11	1	US-07-824-247-19	Sequence 19, Appl
17	21	52.5	11	3	US-08-470-204A-19	Sequence 19, Appl
18	20	50.0	9	1	US-08-215-805A-48	Sequence 48, Appl
19	20	50.0	9	1	US-08-215-805A-61	Sequence 61, Appl
20	20	50.0	9	1	US-08-215-805A-74	Sequence 74, Appl
21	20	50.0	9	3	US-09-139-802-84	Sequence 84, Appl
22	20	50.0	9	4	US-09-659-786-84	Sequence 84, Appl
23	20	50.0	9	4	US-08-926-914-84	Sequence 84, Appl
24	20	50.0	10	6	5196404-18	Patent No. 5196404
25	20	50.0	10	6	5433940-25	Patent No. 5433940
26	20	50.0	12	1	US-08-633-779-3	Sequence 3, Appli
27	20	50.0	12	1	US-08-633-779-5	Sequence 5, Appli
28	20	50.0	12	4	US-09-846-350A-1	Sequence 1, Appli
29	20	50.0	12	4	US-09-569-037-1	Sequence 1, Appli
30	20	50.0	12	4	US-09-569-037-15	Sequence 15, Appl
31	19	47.5	4	1	US-08-329-820-227	Sequence 227, App
32	19	47.5	6	1	US-08-329-820-101	Sequence 101, App
33	19	47.5	6	1	US-08-742-256-13	Sequence 13, Appl
34	19	47.5	6	4	US-09-113-696B-13	Sequence 13, Appl
35	19	47.5	6	6	RE34606-25	Patent No. RE34,60
36	19	47.5	7	1	US-07-940-861-39	Sequence 39, Appl
37	19	47.5	7	1	US-08-459-512-39	Sequence 39, Appl
38	19	47.5	7	1	US-08-798-897-27	Sequence 27, Appl
39	19	47.5	7	2	US-08-244-496-70	Sequence 70, Appl
40	19	47.5	7	2	US-08-978-523-27	Sequence 27, Appl
41	19	47.5	7	2	US-08-459-657-39	Sequence 39, Appl
42	19	47.5	7	2	US-08-460-132-39	Sequence 39, Appl
43	19	47.5	7	5	PCT-US92-02050-39	Sequence 39, Appl
44	19	47.5	8	2	US-08-286-819A-36	Sequence 36, Appl
45	19	47.5	8	3	US-08-980-357-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-459-568-75
; Sequence 75, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-75

Query Match 62.5%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
: :::|||
Db 1 EDLLEGGD 8

```
RESULT 2
US-08-399-411-75
; Sequence 75, Application US/08399411
; Patent No. 5831008
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/399,411
;      FILING DATE:  06-MAR-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-399-411-75

  Query Match             62.5%;  Score 25;  DB 2;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              : :::|||
Db          1 EDLLEGGD 8


RESULT 3
US-08-516-859A-75
; Sequence 75, Application US/08516859A
; Patent No. 6069231
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/516,859A
;      FILING DATE:  18-AUG-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/292,683
;      FILING DATE:  18-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-516-859A-75

  Query Match             62.5%;  Score 25;  DB 3;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              : :::|||
Db          1 EDLLEGGD 8


RESULT 4
US-09-586-472-75
; Sequence 75, Application US/09586472
; Patent No. 6323335
;  GENERAL INFORMATION:
;       APPLICANT: Huang, Shi
;       TITLE OF INVENTION: Retinoblastoma Protein - Interacting
;                           Zinc Finger Proteins
;       NUMBER OF SEQUENCES: 106
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Campbell & Flores LLP
;            STREET: 4370 La Jolla Village Drive, Suite 700
;            CITY: San Diego
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92122
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/586,472
;            FILING DATE: 01-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 09/528,706
;            FILING DATE: 17-MAR-2000
;            APPLICATION NUMBER: US 08/516,859
;            FILING DATE: 18-AUG-1995
;            APPLICATION NUMBER: US 08/399,411
;            FILING DATE: 06-MAR-1995
;            APPLICATION NUMBER: US 08/292,683
;            FILING DATE: 18-AUG-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Campbell, Cathryn A.
;            REGISTRATION NUMBER: 31,815
;            REFERENCE/DOCKET NUMBER: P-LJ 4130
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (619) 535-9001
;            TELEFAX: (619) 535-8949
;  INFORMATION FOR SEQ ID NO: 75:
;       SEQUENCE CHARACTERISTICS:
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; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-586-472-75

Query Match 62.5%; Score 25; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
: :::|||
Db 1 EDLLEGGD 8

RESULT 5
US-09-528-706-75
; Sequence 75, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-528-706-75

Query Match 62.5%; Score 25; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
: :::|||
Db 1 EDLLEGGD 8

RESULT 6
US-08-457-172-1
; Sequence 1, Application US/08457172
; Patent No. 5622837
; GENERAL INFORMATION:
; APPLICANT: Hans Scheefers, Ursula Scheefers-Borchel and
; APPLICANT: Andreas Sziegoleit
; TITLE OF INVENTION: PANCREAS ELASTASE 1-SPECIFIC ANTIBODY, A PROCESS FOR
; TITLE OF INVENTION: OBTAINING IT, AND A TEST KIT CONTAINING SUCH ANTIBODY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,172
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,395
; FILING DATE:
; APPLICATION NUMBER: US 07/969,173
; FILING DATE: 29-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42883/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: pancreatic
US-08-457-172-1

Query Match 62.5%; Score 25; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MIQGGD 8
|: |||
Db 2 MVAGGD 7

RESULT 7
US-08-487-860-62
; Sequence 62, Application US/08487860
; Patent No. 5792456
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
; TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Bldv., Suite 400
; CITY: Los Angeles
; STATE: CA

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;       COUNTRY:  USA
;       ZIP:  90025-3395
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/487,860
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Adriano, Sarah B.
;       REGISTRATION NUMBER:  34,470
;       REFERENCE/DOCKET NUMBER:  30436.16US01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  310-445-1140
;       TELEFAX:  310-445-9031
;   INFORMATION FOR SEQ ID NO:  62:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-487-860-62

  Query Match             57.5%;  Score 23;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 QGGD 8
              ||||
Db          2 QGGD 5


RESULT 8
US-08-953-327-1
; Sequence 1, Application US/08953327
; Patent No. 6033915
;  GENERAL INFORMATION:
;    APPLICANT:  Staud, Roland
;    TITLE OF INVENTION:  MATERIALS AND METHOD FOR THE DETECTION
;    TITLE OF INVENTION:  AND TREATMENT OF WEGENER'S GRANULOMATOSIS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  US
;      ZIP:  32606-6669
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,327
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,701
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  UF-171
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-953-327-1

  Query Match             57.5%;  Score 23;  DB 3;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | :|||  |
Db          3 DGIIQGID 10


RESULT 9
US-09-472-579-1
; Sequence 1, Application US/09472579
; Patent No. 6277955
;  GENERAL INFORMATION:
;    APPLICANT:  Staud, Roland
;    TITLE OF INVENTION:  MATERIALS AND METHOD FOR THE DETECTION
;    TITLE OF INVENTION:  AND TREATMENT OF WEGENER'S GRANULOMATOSIS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Saliwanchik & Saliwanchik
;      STREET:  2421 N.W. 41st Street, Suite A-1
;      CITY:  Gainesville
;      STATE:  FL
;      COUNTRY:  US
;      ZIP:  32606-6669
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/472,579
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,327
;      FILING DATE:
;      APPLICATION NUMBER:  60/028,701
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saliwanchik, David R.
;      REGISTRATION NUMBER:  31,794
;      REFERENCE/DOCKET NUMBER:  UF-171
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (352) 375-8100
;      TELEFAX:  (352) 372-5800
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-472-579-1

  Query Match             57.5%;  Score 23;  DB 3;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | :|||  |
Db          3 DGIIQGID 10


RESULT 10
US-08-215-805A-7
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; Sequence 7, Application US/08215805A
; Patent No. 5559008
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Yung-Fu
;    TITLE OF INVENTION:  LEUKOTOXIN GENE FROM PASTEURELLA
;    TITLE OF INVENTION:  SUIS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/215,805A
;      FILING DATE:  22-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/61 (D-1329A)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Pasteurella suis
;      STRAIN:  5943
;    IMMEDIATE SOURCE:
;      LIBRARY:  P. suis DNA in Bacteriophage lambda-dash
;      CLONE:  (Lambda)yfc33-37
US-08-215-805A-7

  Query Match             55.0%;  Score 22;  DB 1;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 3.8e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              | |||
Db          1 IDGGD 5


RESULT 11
US-08-215-805A-52
; Sequence 52, Application US/08215805A
; Patent No. 5559008
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Yung-Fu
;    TITLE OF INVENTION:  LEUKOTOXIN GENE FROM PASTEURELLA
;    TITLE OF INVENTION:  SUIS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/215,805A
;      FILING DATE:  22-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/61 (D-1329A)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Actinobacillus pleuropneumoniae
US-08-215-805A-52

  Query Match             55.0%;  Score 22;  DB 1;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              ::|||
Db          1 LEGGD 5


RESULT 12
US-08-215-805A-58
; Sequence 58, Application US/08215805A
; Patent No. 5559008
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Yung-Fu
;    TITLE OF INVENTION:  LEUKOTOXIN GENE FROM PASTEURELLA
;    TITLE OF INVENTION:  SUIS
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/215,805A
;      FILING DATE:  22-MAR-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/61 (D-1329A)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
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;      ORGANISM:  Actinobacillus pleuropneumoniae
US-08-215-805A-58

  Query Match             55.0%;  Score 22;  DB 1;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 3.8e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              | |||
Db          1 IHGGD 5


RESULT 13
US-09-296-284-10
; Sequence 10, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
;  APPLICANT:  Choi, Eui-Sung
;  APPLICANT:  Rhee, Sang-Ki
;  APPLICANT:  Lee, Eun-Hae
;  TITLE OF INVENTION:  Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
;  TITLE OF INVENTION:  and Methods of Use Thereof
;  FILE REFERENCE:  1533.0870000
;  CURRENT APPLICATION NUMBER: US/09/296,284A
;  CURRENT FILING DATE:  1999-04-22
;  NUMBER OF SEQ ID NOS:  87
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Gluconobacter suboxydans
US-09-296-284-10

  Query Match             52.5%;  Score 21;  DB 3;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 4.2e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DXMIQGG 7
              | :|| |
Db          4 DALIQRG 10


RESULT 14
US-07-620-426B-19
; Sequence 19, Application US/07620426B
; Patent No. 5298421
;  GENERAL INFORMATION:
;    APPLICANT:  Davies, Huw Maelor
;    APPLICANT:  Pollard, Michael Roman
;    APPLICANT:  Voekler, Toni Alois
;    TITLE OF INVENTION:  Plant Thioesterases
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 KB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 6.0.7
;      SOFTWARE:  MicrosoftWord 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/620,426B
;      FILING DATE:  19901130
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/514,030
;      FILING DATE:  26-APRIL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 70-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  916-753-6313
;      TELEFAX:  916-753-1510
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-620-426B-19

  Query Match             52.5%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGG 7
              ||||
Db          3 IQGG 6


RESULT 15
US-07-662-007B-19
; Sequence 19, Application US/07662007B
; Patent No. 5344771
;  GENERAL INFORMATION:
;    APPLICANT:  Davies, Huw Maelor
;    APPLICANT:  Pollard, Michael Roman
;    APPLICANT:  Voekler, Toni Alois
;    APPLICANT:  Thompson, Gregory A.
;    TITLE OF INVENTION:  Plant Thioesterases
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 KB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 6.0.7
;      SOFTWARE:  MicrosoftWord 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/662,007B
;      FILING DATE:  19910408
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/514,030
;      FILING DATE:  26-APR-1990
;      APPLICATION NUMBER:  07/620,426
;      FILING DATE:  30-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      REFERENCE/DOCKET NUMBER:  CGNE 70-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  916-753-6313
;      TELEFAX:  916-753-1510
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-662-007B-19

  Query Match             52.5%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+02;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 IQGG 7
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Db          3 IQGG 6
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Search completed: October 21, 2004, 07:29:29
Job time : 22.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	92.5	9	15	US-10-447-161-85	Sequence 85, Appl
2	37	92.5	9	16	US-10-788-016-2	Sequence 2, Appli
3	37	92.5	9	16	US-10-788-016-9	Sequence 9, Appli
4	22	55.0	12	16	US-10-128-520-96	Sequence 96, Appl
5	21	52.5	9	14	US-10-210-148-9	Sequence 9, Appli
6	21	52.5	9	14	US-10-210-148-14	Sequence 14, Appl
7	21	52.5	11	14	US-10-194-985-32	Sequence 32, Appl
8	21	52.5	11	15	US-10-356-257-161	Sequence 161, App
9	20	50.0	5	14	US-10-076-047A-124	Sequence 124, App
10	20	50.0	5	16	US-10-620-052A-50	Sequence 50, Appl
11	20	50.0	9	9	US-09-765-086-84	Sequence 84, Appl
12	20	50.0	9	9	US-09-912-787-35	Sequence 35, Appl
13	20	50.0	9	13	US-10-014-326-21	Sequence 21, Appl
14	20	50.0	9	14	US-10-264-374-84	Sequence 84, Appl
15	20	50.0	9	14	US-10-375-992-84	Sequence 84, Appl
16	20	50.0	9	14	US-10-137-867-10	Sequence 10, Appl
17	20	50.0	9	15	US-10-264-374-84	Sequence 84, Appl
18	20	50.0	9	16	US-10-375-992-84	Sequence 84, Appl
19	20	50.0	10	9	US-09-846-350-1	Sequence 1, Appli
20	20	50.0	11	9	US-09-846-342-1	Sequence 1, Appli
21	20	50.0	12	9	US-09-845-725-1	Sequence 1, Appli
22	20	50.0	12	14	US-10-148-687-32	Sequence 32, Appl
23	19	47.5	4	14	US-10-084-388A-2	Sequence 2, Appli
24	19	47.5	5	14	US-10-076-047A-130	Sequence 130, App
25	19	47.5	5	15	US-10-436-549-36	Sequence 36, Appl
26	19	47.5	5	16	US-10-712-425-36	Sequence 36, Appl
27	19	47.5	5	17	US-10-723-933-96	Sequence 96, Appl
28	19	47.5	6	9	US-09-113-696B-13	Sequence 13, Appl
29	19	47.5	6	17	US-10-723-933-25	Sequence 25, Appl
30	19	47.5	6	17	US-10-723-933-97	Sequence 97, Appl
31	19	47.5	6	17	US-10-723-933-120	Sequence 120, App
32	19	47.5	7	14	US-10-190-082-84	Sequence 84, Appl
33	19	47.5	7	14	US-10-190-082-159	Sequence 159, App
34	19	47.5	7	16	US-10-481-180-426	Sequence 426, App
35	19	47.5	7	17	US-10-723-933-7	Sequence 7, Appli
36	19	47.5	7	17	US-10-723-933-12	Sequence 12, Appl
37	19	47.5	7	17	US-10-723-933-26	Sequence 26, Appl
38	19	47.5	7	17	US-10-723-933-88	Sequence 88, Appl
39	19	47.5	7	17	US-10-723-933-98	Sequence 98, Appl
40	19	47.5	8	15	US-10-462-452-445	Sequence 445, App
41	19	47.5	8	15	US-10-601-953-574	Sequence 574, App
42	19	47.5	8	16	US-10-322-266-446	Sequence 446, App
43	19	47.5	8	17	US-10-723-933-11	Sequence 11, Appl
44	19	47.5	8	17	US-10-723-933-27	Sequence 27, Appl
45	19	47.5	8	17	US-10-723-933-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-447-161-85
; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match 92.5%; Score 37; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DFMIQGGD 8
```

RESULT 2
US-10-788-016-2
; Sequence 2, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo

```
;  TITLE OF INVENTION: Desensitizers
;  FILE REFERENCE: 3190-049
;  CURRENT APPLICATION NUMBER: US/10/788,016
;  CURRENT FILING DATE:  2004-02-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/08641
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: JP P2001-260046
;  PRIOR FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
;   OTHER INFORMATION: to the 99th residue of cyclophillin B
US-10-788-016-2

  Query Match             92.5%;  Score 37;  DB 16;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DFMIQGGD 8


RESULT 3
US-10-788-016-9
; Sequence 9, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
;  APPLICANT: ITOH, Kyogo
;  TITLE OF INVENTION: Desensitizers
;  FILE REFERENCE: 3190-049
;  CURRENT APPLICATION NUMBER: US/10/788,016
;  CURRENT FILING DATE:  2004-02-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/08641
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: JP P2001-260046
;  PRIOR FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
;   OTHER INFORMATION: residues from the 91st residue to the 99th residue of
;   OTHER INFORMATION: cyclophillin B
US-10-788-016-9

  Query Match             92.5%;  Score 37;  DB 16;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ||||||
Db          1 DYMIQGGD 8


RESULT 4
US-10-128-520-96
; Sequence 96, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
;  APPLICANT: PAN et al.
;  TITLE OF INVENTION: Human TIMP-1 Antibodies
;  FILE REFERENCE: 02973.00073
;  CURRENT APPLICATION NUMBER: US/10/128,520
;  CURRENT FILING DATE:  2002-04-24
;  PRIOR APPLICATION NUMBER: US 60/285,683
;  PRIOR FILING DATE: 2001-04-24
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-128-520-96

  Query Match             55.0%;  Score 22;  DB 16;  Length 12;
  Best Local Similarity   37.5%;  Pred. No. 9.7e+02;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DXMIQGGD 8
              | ::|| :
Db          5 DQLLQGSE 12


RESULT 5
US-10-210-148-9
; Sequence 9, Application US/10210148
; Publication No. US20030171280A1
; GENERAL INFORMATION:
;  APPLICANT: Soderstrom, Karl Petter
;  TITLE OF INVENTION: Compositions And Methods For Mcdulation Of Immune Response
;  FILE REFERENCE: TROM0002
;  CURRENT APPLICATION NUMBER: US/10/210,148
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: PCT/US02/24311
;  PRIOR FILING DATE: 2002-07-31
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-210-148-9

  Query Match             52.5%;  Score 21;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |:|| |
Db          2 MLQGVD 7


RESULT 6
US-10-210-148-14
; Sequence 14, Application US/10210148
; Publication No. US20030171280A1
; GENERAL INFORMATION:
;  APPLICANT: Soderstrom, Karl Petter
;  TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
;  FILE REFERENCE: TROM0002
;  CURRENT APPLICATION NUMBER: US/10/210,148
;  CURRENT FILING DATE:  2002-07-31
;  PRIOR APPLICATION NUMBER: PCT/US02/24311
;  PRIOR FILING DATE: 2002-07-31
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-210-148-14

  Query Match             52.5%;  Score 21;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
```

```
Db          2 MLQGVD 7


RESULT 7
US-10-194-985-32
; Sequence 32, Application US/10194985
; Publication No. US20030105287A1
; GENERAL INFORMATION:
;  APPLICANT: Schaeffer, Michael
;  APPLICANT:  Schneiderbauer, Michaela
;  APPLICANT:  Weidler, Sascha
;  APPLICANT:  Hallek, Michael
;  APPLICANT:  GSF Forschungszentrum fuer Umwelt und Gesundheit GmbH
;  TITLE OF INVENTION: Inhibition of the Proliferation of Cells of the
;  TITLE OF INVENTION:  Multiple Myeloma
;  FILE REFERENCE: 080345-000100US
;  CURRENT APPLICATION NUMBER: US/10/194,985
;  CURRENT FILING DATE:  2002-07-12
;  PRIOR APPLICATION NUMBER: DE 19941897.7
;  PRIOR FILING DATE: 1999-09-02
;  PRIOR APPLICATION NUMBER: US 09/625,225
;  PRIOR FILING DATE: 2000-07-24
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:P8 peptide
;   OTHER INFORMATION: subfragment of Hck binding region of gp130
US-10-194-985-32

  Query Match             52.5%;  Score 21;  DB 14;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              : |||
Db          2 VDGGD 6


RESULT 8
US-10-356-257-161
; Sequence 161, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
;  APPLICANT: LAZARUS, ROBERT A.
;  APPLICANT:  MAUN, HENRY R.
;  TITLE OF INVENTION: FVIIa Antagonists
;  FILE REFERENCE: P1950R1
;  CURRENT APPLICATION NUMBER: US/10/356,257
;  CURRENT FILING DATE:  2003-01-30
;  PRIOR APPLICATION NUMBER: US 60/355,420
;  PRIOR FILING DATE: 2002-02-06
;  NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 161
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is synthesized
US-10-356-257-161

  Query Match             52.5%;  Score 21;  DB 15;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              |::||
Db          7 MVRGG 11


RESULT 9
US-10-076-047A-124
; Sequence 124, Application US/10076047A
; Publication No. US20030152935A1
; GENERAL INFORMATION:
;  APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
;  TITLE OF INVENTION: Proteins, Genes and Their Use for
;  TITLE OF INVENTION:  Diagnosis and Treatment of Breast Cancer
;  FILE REFERENCE: 2543-1-026
;  CURRENT APPLICATION NUMBER: US/10/076,047A
;  CURRENT FILING DATE:  2002-02-13
;  PRIOR APPLICATION NUMBER: GB 9919258.5
;  PRIOR FILING DATE: 1999-08-13
;  PRIOR APPLICATION NUMBER: GB 0007754.5
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: PCT/GB00/03143
;  PRIOR FILING DATE: 2000-08-14
;  NUMBER OF SEQ ID NOS: 351
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-076-047A-124

  Query Match             50.0%;  Score 20;  DB 14;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              :|:||
Db          1 LIEGG 5


RESULT 10
US-10-620-052A-50
; Sequence 50, Application US/10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
;  APPLICANT: Hitoshi, Yasumichi
;  APPLICANT:  Jenkins, Yonchu
;  APPLICANT:  Markovtsov, Vadim
;  APPLICANT:  Rigel Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Modulators of Cellular Proliferation
;  FILE REFERENCE: 021044-004010US
;  CURRENT APPLICATION NUMBER: US/10/620,052A
;  CURRENT FILING DATE:  2003-07-14
;  PRIOR APPLICATION NUMBER: US 60/395,443
;  PRIOR FILING DATE: 2002-07-12
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: peptide
US-10-620-052A-50

  Query Match             50.0%;  Score 20;  DB 16;  Length 5;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 QGGD 8
              :|||
Db          1 EGGD 4


RESULT 11
US-09-765-086-84
; Sequence 84, Application US/09765086
```

; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-84

Query Match 50.0%; Score 20; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 MIQGGD 8
              |:: ||
Db          3 MVRDGD 8
```

RESULT 12
US-09-912-787-35
; Sequence 35, Application US/09912787
; Patent No. US20020119149A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBSEN, Bent Karsten
; APPLICANT: BOULTER, Jonathan Michael
; TITLE OF INVENTION: Multivalent T Cell Receptor Complexes
; FILE REFERENCE: 102286.410DIV
; CURRENT APPLICATION NUMBER: US/09/912,787
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 09/334,969
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/GB99 01583
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9810759.2
; PRIOR FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: GB 9821129.5
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: New
; OTHER INFORMATION: N-terminal amino acid sequence of the truncated
; OTHER INFORMATION: Vbeta17 chain of the human JM22 Influenza Matrix
; OTHER INFORMATION: peptide/HLA-A0201 restricted TCR.
US-09-912-787-35

Query Match 50.0%; Score 20; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 MIQGG 7
              |: ||
Db          1 MVDGG 5
```

RESULT 13
US-10-014-326-21
; Sequence 21, Application US/10014326
; Publication No. US20020142389A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBSEN, Bent Karsten
; APPLICANT: BELL, John Irving
; APPLICANT: GAO, George Fu
; APPLICANT: WILLCOX, Benjamin Ernest
; APPLICANT: BOULTER, Jonathan Michael
; TITLE OF INVENTION: Soluble T Cell Receptor
; FILE REFERENCE: 102286.409
; CURRENT APPLICATION NUMBER: US/10/014,326
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/335,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB/9810759.2
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: New N-terminal amino acid sequence of truncated V
; OTHER INFORMATION: beta17 chain of the human JM22 Influenza matrix
; OTHER INFORMATION: peptide-HLA-A0201 restricted TCR. (Figure 9B).
; OTHER INFORMATION: Description of Artificial Sequence:New N-terminal
; OTHER INFORMATION: amino acid sequence of truncated V beta17 chain of
; OTHER INFORMATION: the JM22 Influenza matrix peptide-HLA-A0201
; OTHER INFORMATION: restricted TCR. (Figure 9A)
US-10-014-326-21

Query Match 50.0%; Score 20; DB 13; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 MIQGG 7
              |: ||
Db          1 MVDGG 5
```

RESULT 14
US-10-264-374-84
; Sequence 84, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-84

```
  Query Match             50.0%;  Score 20;  DB 14;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |:: ||
Db          3 MVRDGD 8


RESULT 15
US-10-375-992-84
; Sequence 84, Application US/10375992
; Publication No. US20030152578A1
;   GENERAL INFORMATION:
;        APPLICANT: Ruoslahti, Erkki
;                   Pasqualini, Renata
;        TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
;                            Derived Therefrom, and Methods of Using Same
;        NUMBER OF SEQUENCES: 199
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Campbell & Flores
;             STREET: 4370 La Jolla Village Drive, Suite 700
;             CITY: San Diego
;             STATE: California
;             COUNTRY: United States
;             ZIP: 92122
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/375,992
;             FILING DATE: 27-Feb-2003
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/926,914
;             FILING DATE: 10-SEP-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Campbell, Cathryn A.
;             REGISTRATION NUMBER: 31,815
;             REFERENCE/DOCKET NUMBER: P-LJ 2725
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (619) 535-9001
;             TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 84:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             TOPOLOGY: both
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-375-992-84

  Query Match             50.0%;  Score 20;  DB 14;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |:: ||
Db          3 MVRDGD 8


Search completed: October 21, 2004, 07:33:42
Job time : 62.75 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	50.0	12	2	S43170	kinesin light chai
2	19	47.5	11	2	B60769	Ig H2 chain - Paci
3	18	45.0	7	2	PT0542	T-cell receptor be
4	18	45.0	9	2	QDRB	delta sleep-induci
5	18	45.0	11	2	PH1343	Ig heavy chain DJ
6	18	45.0	11	2	S60354	retinal oxidase -
7	18	45.0	11	2	PN0044	protein kinase C i
8	18	45.0	11	2	PT0218	T-cell receptor be
9	18	45.0	11	2	I41946	T-cell receptor ga
10	18	45.0	11	2	A61575	Trimeresurus serin
11	17	42.5	3	3	A23751	spinal cord peptid
12	17	42.5	9	1	YFPG	thymic factor - pi
13	17	42.5	9	2	A60957	thymocyte growth p
14	17	42.5	11	2	S57575	T cell receptor V-
15	17	42.5	11	2	D37196	bradykinin-potenti
16	17	42.5	11	4	S19015	hypothetical prote
17	17	42.5	12	2	PH1458	T-cell receptor be
18	16	40.0	12	2	A61309	glycoprotein hormo
19	16	40.0	12	2	S65730	hemoglobin, extrac
20	16	40.0	12	2	T46794	hypothetical prote
21	15	37.5	4	2	S47552	ubiquitin - rat
22	15	37.5	4	2	S09478	globulin IV alpha
23	15	37.5	7	2	S58797	serine/threonine-s
24	15	37.5	7	4	S15597	orf 4 rara 5'-regi
25	15	37.5	8	2	A31570	angiotensin-conver
26	15	37.5	9	2	I50633	c-rel protein - ch
27	15	37.5	10	2	PC2172	triacylglycerol li
28	15	37.5	10	2	PT0309	Ig heavy chain CRD
29	15	37.5	10	2	B56899	serum heterodimer,
30	15	37.5	11	2	A38590	transforming prote
31	15	37.5	12	2	S26544	T-cell receptor be
32	15	37.5	12	2	PA0030	protein QA300025 -
33	15	37.5	12	2	E44787	calliMIRFamide 1 -
34	15	37.5	12	2	A53252	pollen major aller
35	14	35.0	5	2	B61168	cocoonase (EC 3.4.
36	14	35.0	5	2	I50385	myosin light chain
37	14	35.0	7	2	E61491	seed protein ws-5
38	14	35.0	7	2	PT0667	T-cell receptor be
39	14	35.0	7	2	PT0586	T-cell receptor be
40	14	35.0	7	2	T09512	NADH2 dehydrogenas
41	14	35.0	8	2	C39690	neural cell adhesi
42	14	35.0	9	2	S66608	quinoline 2-oxidor
43	14	35.0	9	2	A53797	3',5'-cyclic-GMP p
44	14	35.0	9	2	A57444	neuropeptide Grb-A
45	14	35.0	9	2	B57444	neuropeptide Grb-A

ALIGNMENTS

RESULT 1
S43170
kinesin light chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: S43170
R;Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
submitted to the EMBL Data Library, December 1992
A;Description: Promoter first exon/intron characterization and chromosomal location of th
A;Reference number: S43170
A;Accession: S43170
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <CHE>
A;Cross-references: UNIPROT:Q13865; EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g46878

Query Match 50.0%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 MIQGG 7
              |::||
Db          1 MLRGG 5
```

RESULT 2
B60769
Ig H2 chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C;Accession: B60769
R;Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A;Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A;Reference number: A60769; MUID:91060965; PMID:2123225
A;Accession: B60769
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HAN>

Query Match 47.5%; Score 19; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DXMIQ 5
              | |||
Db          5 DFMIQ 9
```

RESULT 3
PT0542
T-cell receptor beta chain V-D-J region (126-1BA) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0542
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0542
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 3 GGD 5

RESULT 4
QDRB
delta sleep-inducing peptide - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C;Accession: A01422
R;Monnier, M.; Dudler, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.
Experientia 33, 548-552, 1977
A;Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original
A;Reference number: A01422; MUID:77185324; PMID:862769
A;Accession: A01422
A;Molecule type: protein
A;Residues: 1-9 <MON>
A;Cross-references: UNIPROT:P01158
C;Comment: This peptide was obtained from dialysates of occipital venous sinus blood fro
of recipient rabbits, it induces spindle and delta EEG activity and reduced motor activ

Query Match 45.0%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 3 GGD 5

RESULT 5
PH1343
Ig heavy chain DJ region (clone C100-91) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1343
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1343
A;Molecule type: DNA
A;Residues: 1-11 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 1 GGD 3

RESULT 6
S60354
retinal oxidase - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S60354
R;Huang, D.Y.; Ichikawa, Y.
Biochim. Biophys. Acta 1243, 431-436, 1995
A;Title: Identification of essential lysyl and cysteinyl residues, and the amino acid sec
A;Reference number: S60354; MUID:95244596; PMID:7727518
A;Accession: S60354
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HUA>

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 1 GGD 3

RESULT 7
PN0044
protein kinase C inhibitor I - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0044
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroh
A;Reference number: PN0041
A;Accession: PN0044
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked
C;Keywords: brain

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 8 GGD 10

RESULT 8
PT0218
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0218
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0218
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGGD 8
|||:
Db 5 QGGN 8

RESULT 9
I41946
T-cell receptor gamma chain (5t.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: I41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: I41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 5 GGD 7

RESULT 10
A61575
Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)
N;Alternate names: hemorrhagic toxin
C;Species: Trimeresurus elegans (Sakishima habu)
C;Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: A61575
R;Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.
Int. J. Biochem. 23, 73-78, 1991
A;Title: Isolation and characterization of hemorrhagic toxin from the venom of Trimeresu
A;Reference number: A61575; MUID:91216327; PMID:2022298
A;Accession: A61575
A;Molecule type: protein
A;Residues: 1-11 <NIK>
C;Keywords: hydrolase; serine proteinase; venom

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
||||
Db 3 GGD 5

RESULT 11
A23751
spinal cord peptide SCP-4 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K
Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
A;Accession: A23751
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-3 <HSI>

Query Match 42.5%; Score 17; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
|||
Db 1 QGG 3

RESULT 12
YFPG
thymic factor - pig
N;Alternate names: FTS (facteur thymique serique)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01523; A60983
R;Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A;Title: Structural study of circulating thymic factor: a peptide isolated from pig serun
A;Reference number: A01523; MUID:78026571; PMID:914862
A;Accession: A01523
A;Molecule type: protein
A;Residues: 1-9 <PLE>
A;Cross-references: UNIPROT:P01255
R;Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A;Title: Biochemical characterisation of a serum thymic factor.
A;Reference number: A60983; MUID:77123829; PMID:300146
A;Accession: A60983
A;Molecule type: protein
A;Residues: 'Z',2-4,'Z',6-9 <BAC>
C;Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C;Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modificat
C;Superfamily: thymic factor
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.5%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
|||
Db 5 QGG 7

RESULT 13
A60957
thymocyte growth peptide - sheep
N;Contains: FTS (facteur thymique serique)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A60957
R;Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A;Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship t
A;Reference number: A60957; MUID:91064427; PMID:2249004
A;Accession: A60957
A;Molecule type: protein
A;Residues: 1-9 <ERN>
A;Cross-references: UNIPROT:Q7M3C5
C;Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C;Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca
r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hig
C;Superfamily: thymic factor
C;Keywords: blocked amino end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experime

Query Match 42.5%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
|||
Db 5 QGG 7

RESULT 14

S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A;Reference number: S57494
A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor

  Query Match 42.5%; Score 17; DB 2; Length 11;
  Best Local Similarity 100.0%; Pred. No. 1.5e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
   |||
Db 4 QGG 6

RESULT 15
D37196
bradykinin-potentiating peptide 4 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: D37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: D37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
A;Cross-references: UNIPROT:P30424
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

  Query Match 42.5%; Score 17; DB 2; Length 11;
  Best Local Similarity 100.0%; Pred. No. 1.5e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
   |||
Db 1 QGG 3

Search completed: October 21, 2004, 07:27:58
Job time : 16.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	57.5	7	2	Q63480	Q63480 rattus norv
2	22	55.0	12	2	Q9H3W2	Q9h3w2 homo sapien
3	21	52.5	12	2	Q70Y58	Q70y58 clinopodium
4	21	52.5	12	2	CAD45546	Cad45546 clinopodi
5	20	50.0	12	2	Q13865	Q13865 homo sapien
6	19	47.5	7	2	O55184	O55184 rattus norv
7	19	47.5	11	2	Q70Y98	Q70y98 capitanopsi
8	19	47.5	11	2	CAD45456	Cad45456 capitanop
9	18	45.0	9	1	DSIP_RABIT	P01158 oryctolagus
10	18	45.0	9	2	Q6LDH6	Q6ldh6 rattus norv
11	18	45.0	9	2	AAA40600	Aaa40600 rattus no
12	18	45.0	10	2	Q51812	Q51812 plasmid f.
13	18	45.0	12	2	Q9H1Z6	Q9h1z6 homo sapien
14	18	45.0	12	2	Q9N2B8	Q9n2b8 pongo pygma
15	18	45.0	12	2	Q9N2B9	Q9n2b9 gorilla gor
16	18	45.0	12	2	Q9N2C0	Q9n2c0 pan troglod
17	18	45.0	12	2	O54226	O54226 saccharopol
18	17	42.5	7	1	ASCL_ALLAS	P84071 allium asca
19	17	42.5	9	1	THYF_PIG	P01255 sus scrofa
20	17	42.5	9	2	Q7M3C5	Q7m3c5 ovis aries
21	17	42.5	10	2	Q6LCI4	Q6lci4 homo sapien
22	17	42.5	10	2	Q96QA7	Q96qa7 homo sapien
23	17	42.5	10	2	AAD14854	Aad14854 homo sapi
24	17	42.5	11	1	BPP4_BOTIN	P30424 bothrops in
25	17	42.5	11	2	Q70Y64	Q70y64 plectranthu
26	17	42.5	11	2	Q47420	Q47420 escherichia
27	17	42.5	11	2	CAD45529	Cad45529 plectrant
28	16	40.0	10	1	ESTA_SCHGA	P81012 schizaphis
29	16	40.0	10	2	Q8UVW2	Q8uvw2 oreochromis
30	16	40.0	12	2	Q7M0A7	Q7m0a7 cricetidae
31	16	40.0	12	2	Q8UVV8	Q8uvv8 squalus aca
32	16	40.0	12	2	Q8UVW0	Q8uvw0 rana catesb
33	15	37.5	8	1	ACI_THUAL	P18691 thunnus alb
34	15	37.5	8	2	Q9P0K3	Q9p0k3 homo sapien
35	15	37.5	9	2	Q9BQT4	Q9bqt4 homo sapien
36	15	37.5	9	2	Q6YF34	Q6yf34 rattus norv
37	15	37.5	9	2	Q92009	Q92009 gallus gall
38	15	37.5	9	2	AAN87279	Aan87279 rattus no
39	15	37.5	10	2	Q6X2S9	Q6x2s9 homo sapien
40	15	37.5	10	2	Q85V66	Q85v66 eucalyptus
41	15	37.5	10	2	Q7LZJ7	Q7lzj7 carcharhinu
42	15	37.5	10	2	Q7ZZJ2	Q7zzj2 motacilla f
43	15	37.5	10	2	AAP83315	Aap83315 homo sapi
44	15	37.5	11	2	Q7ZZI6	Q7zzi6 motacilla f
45	15	37.5	11	2	Q7ZZI9	Q7zzi9 motacilla f

ALIGNMENTS

RESULT 1
Q63480
ID Q63480 PRELIMINARY; PRT; 7 AA.
AC Q63480;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
DR EMBL; U59125; AAB02827.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 57.5%; Score 23; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 IQGGD 8
              |:|||
Db          2 IRGGD 6
```

RESULT 2
Q9H3W2
ID Q9H3W2 PRELIMINARY; PRT; 12 AA.
AC Q9H3W2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TRE17 protein.
GN Name=TRE17 gene;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010310; PubMed=8406013;
RA Onno M., Nakamura T., Hillova J., Hill M.;

```
RT   "Identification of novel sequences in the repertoire of hypervariable
RT   TRE17 genes from immortalized nonmalignant and malignant human
RT   keratinocytes.";
RL   Gene 131:209-215(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93228825; PubMed=8471161;
RA   Onno M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.;
RT   "Human TRE17 oncogene is generated from a family of homologous
RT   polymorphic sequences by single-base changes.";
RL   DNA Cell Biol. 12:107-118(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hillova F.;
RL   Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X71371; CAC16150.1; -.
SQ   SEQUENCE   12 AA;  1252 MW;  6E17AFDE83ADD87B CRC64;

  Query Match             55.0%;  Score 22;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |::| |
Db          3 MVEGAD 8


RESULT 3
Q70Y58
ID   Q70Y58      PRELIMINARY;      PRT;    12 AA.
AC   Q70Y58;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   Name=rps16;
OS   Clinopodium vulgare subsp. arundanum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium.
OX   NCBI_TaxID=204223;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019625;
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505426; CAD45546.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1353 MW;  D43D1B51AF587866 CRC64;

  Query Match             52.5%;  Score 21;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGG 7
              ||||
Db          4 IQGG 7


RESULT 4
CAD45546
ID   CAD45546    PRELIMINARY;      PRT;    12 AA.
AC   CAD45546;
DT   14-MAR-2004 (TrEMBLrel. 27, Created)
DT   14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   RPS16.
OS   Clinopodium vulgare subsp. arundanum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium;
OC   Clinopodium vulgare.
OX   NCBI_TaxID=204223;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505426; CAD45546.1; -.
KW   Chloroplast; Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1353 MW;  D43D1B51AF587866 CRC64;

  Query Match             52.5%;  Score 21;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGG 7
              ||||
Db          4 IQGG 7


RESULT 5
Q13865
ID   Q13865      PRELIMINARY;      PRT;    12 AA.
AC   Q13865;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Kinesin light chain.
GN   Name=beta-kinesin;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97101110; PubMed=8945637;
RA   Chernajovsky Y., Brown A., Jones T.A.;
RT   "Promoter first exon/intron characterization and chromosomal location
RT   of the human light chain (beta) kinesin gene.";
RL   DNA Cell Biol. 15:965-974(1996).
DR   EMBL; X69658; CAA49349.1; -.
DR   PIR; S43170; S43170.
SQ   SEQUENCE   12 AA;  1274 MW;  3FB8D34EE165A5B8 CRC64;

  Query Match             50.0%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 3.5e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              |::||
Db          1 MLRGG 5


RESULT 6
O55184
ID   O55184      PRELIMINARY;      PRT;     7 AA.
AC   O55184;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orphan receptor TR4-NS (Fragment).
```

```
GN   Name=TR4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96198747; PubMed=8612486;
RA   Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA   Detera-Wadleigh S.D.;
RT   "Splice variants of rat TR4 orphan receptor: differential expression
RT   of novel sequences in the 5'-untranslated region and C-terminal
RT   domain.";
RL   Endocrinology 137:1562-1571(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96299786; PubMed=8661150;
RA   Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT   "New variants of the human and rat nuclear hormone receptor, TR4:
RT   expression and chromosomal localization of the human gene.";
RL   Genomics 35:361-366(1996).
DR   EMBL; U59454; AAB91433.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  663 MW;  6DDAA8787EB05350 CRC64;

  Query Match             47.5%;  Score 19;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              | |||
Db          2 ICGGD 6


RESULT 7
Q70Y98
ID   Q70Y98      PRELIMINARY;      PRT;    11 AA.
AC   Q70Y98;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   Name=rps16;
OS   Capitanopsis angustifolia.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Capitanopsis.
OX   NCBI_TaxID=204110;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019625;
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505333; CAD45456.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1161 MW;  2AB3C5D9BEAB5878 CRC64;

  Query Match             47.5%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 5.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              : |||
Db          1 LFQGG 5


RESULT 8
CAD45456
ID   CAD45456    PRELIMINARY;      PRT;    11 AA.
AC   CAD45456;
DT   14-MAR-2004 (TrEMBLrel. 27, Created)
DT   14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   RPS16.
OS   Capitanopsis angustifolia.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Capitanopsis.
OX   NCBI_TaxID=204110;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505333; CAD45456.1; -.
KW   Chloroplast; Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1161 MW;  2AB3C5D9BEAB5878 CRC64;

  Query Match             47.5%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 5.2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              : |||
Db          1 LFQGG 5


RESULT 9
DSIP_RABIT
ID   DSIP_RABIT     STANDARD;      PRT;     9 AA.
AC   P01158;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Delta sleep-inducing peptide (DSIP).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77185324; PubMed=862769;
RA   Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA   Schoenenberger G.A.;
RT   "The delta sleep inducing peptide (DSIP). Comparative properties of
RT   the original and synthetic nonapeptide.";
RL   Experientia 33:548-552(1977).
RN   [2]
RP   SEQUENCE, AND SYNTHESIS.
RX   MEDLINE=79054421; PubMed=568769;
RA   Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT   "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
RT   analysis, sequence, synthesis and activity of the nonapeptide.";
RL   Pflugers Arch. 376:119-129(1978).
RN   [3]
RP   REVIEW.
RX   MEDLINE=87175129; PubMed=3550726;
RA   Graf M.V., Kastin A.J.;
RT   "Delta-sleep-inducing peptide (DSIP): an update.";
```

```
RL   Peptides 7:1165-1187(1986).
CC   -!- FUNCTION: When infused into the mesodiencephalic ventricle of
CC       recipient rabbits induces spindle and delta EEG activity and
CC       reduced motor activities.
CC   -!- MISCELLANEOUS: This peptide was obtained from dialysates of
CC       occipital venous sinus blood from rabbits kept asleep by electric
CC       stimulation of the thalamus.
CC   -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 8 of March 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".
DR   PIR; A01422; QDRB.
KW   Direct protein sequencing.
SQ   SEQUENCE   9 AA;  849 MW;  DDD365BDDAA8787D CRC64;

  Query Match             45.0%;  Score 18;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGD 8
              |||
Db          3 GGD 5


RESULT 10
Q6LDH6
ID   Q6LDH6      PRELIMINARY;      PRT;     9 AA.
AC   Q6LDH6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   11-beta-hydroxysteroid dehydrogenase (EC 1.1.1.146) (Fragment).
GN   Name=11-HSDIB;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=92129344; PubMed=1733955;
RA   Krozowski Z., Obeyesekere V., Smith R., Mercer W.;
RT   "Tissue-specific expression of an 11-beta-hydroxysteroid dehydrogenase
RT   with a truncated N-terminal domain: A potential mechanism for
RT   differential intracellular localization within mineralocorticoid
RT   target cells.";
RL   J. Biol. Chem. 267:2569-2574(1992).
DR   EMBL; M77835; AAA40600.1; -.
DR   GO; GO:0003845; F:11-beta-hydroxysteroid dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
KW   Oxidoreductase.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1015 MW;  41F942C3333866D7 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQG 6
              |:||
Db          1 MLQG 4


RESULT 11
AAA40600
ID   AAA40600    PRELIMINARY;      PRT;     9 AA.
AC   AAA40600;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   11-beta-hydroxysteroid dehydrogenase (EC 1.1.1.146) (Fragment).
GN   11-HSDIB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=92129344; PubMed=1733955;
RA   Krozowski Z., Obeyesekere V., Smith R., Mercer W.;
RT   "Tissue-specific expression of an 11-beta-hydroxysteroid dehydrogenase
RT   with a truncated N-terminal domain: A potential mechanism for
RT   differential intracellular localization within mineralocorticoid
RT   target cells.";
RL   J. Biol. Chem. 267:2569-2574(1992).
DR   EMBL; M77835; AAA40600.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1015 MW;  41F942C3333866D7 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQG 6
              |:||
Db          1 MLQG 4


RESULT 12
Q51812
ID   Q51812      PRELIMINARY;      PRT;    10 AA.
AC   Q51812;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   DNA helicase (Fragment).
GN   Name=traI;
OS   Plasmid F.
OG   Plasmid F.
OC   plasmids.
OX   NCBI_TaxID=2465;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92009201; PubMed=1916281;
RA   Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;
RT   "Sequence and conservation of genes at the distal end of the transfer
RT   region on plasmids F and R6-5.";
RL   Gene 104:85-90(1991).
DR   EMBL; M38047; AAA98090.1; -.
DR   GO; GO:0004386; F:helicase activity; IEA.
KW   Helicase; Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1088 MW;  59A3047731A33B13 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGD 8
              |||
Db          8 GGD 10


RESULT 13
Q9H1Z6
ID   Q9H1Z6      PRELIMINARY;      PRT;    12 AA.
AC   Q9H1Z6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Estrogen receptor 1 (Fragment).
GN   Name=ESR1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RA   Gonzalez-Gomez F., Vergara F., Pedrosa C., Ramirez J.P.,
RA   Castilla J.A., Yoldi A., Ruiz A., Real L.M.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF326912; AAG42501.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1385 MW;  09168BCB76C41404 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   57.1%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DXMIQGG 7
              |   |||
Db          4 DNRRQGG 10


RESULT 14
Q9N2B8
ID   Q9N2B8      PRELIMINARY;      PRT;    12 AA.
AC   Q9N2B8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Indolethylamine N-methyltransferase (Fragment).
GN   Name=INMT;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kitano T., Kobayakawa H., Saitou N.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB041365; BAA94454.1; -.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Methyltransferase; Transferase.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1290 MW;  CF079554917861A9 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGD 8
              |||
Db          7 GGD 9


RESULT 15
Q9N2B9
ID   Q9N2B9      PRELIMINARY;      PRT;    12 AA.
AC   Q9N2B9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Indolethylamine N-methyltransferase (Fragment).
GN   Name=INMT;
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kitano T., Kobayakawa H., Saitou N.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB041364; BAA94453.1; -.
DR   GO; GO:0008168; F:methyltransferase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
KW   Methyltransferase; Transferase.
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1289 MW;  CF0798E2917861A9 CRC64;

  Query Match             45.0%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGD 8
              |||
Db          7 GGD 9


Search completed: October 21, 2004, 07:26:49
Job time : 88 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	100.0	9	3	AAY69962	Aay69962 Human cyc
2	50	100.0	9	4	AAB46946	Aab46946 Human cyc
3	46	92.0	9	3	AAY69921	Aay69921 Human cyc
4	46	92.0	9	4	AAB46930	Aab46930 Human cyc
5	46	92.0	9	4	AAG68088	Aag68088 Antitumou
6	46	92.0	9	5	ABG79075	Abg79075 Human Cyp
7	46	92.0	9	6	ABR84373	Abr84373 Human Cyp
8	46	92.0	9	7	ADC17701	Adc17701 Cyclophil
9	46	92.0	9	8	ADG89641	Adg89641 Class I H
10	36	72.0	9	3	AAY69960	Aay69960 Human cyc
11	31	62.0	10	2	AAR96521	Aar96521 Hepatitis
12	31	62.0	11	4	AAB82292	Aab82292 Phosphory
13	29	58.0	9	3	AAY69959	Aay69959 Human cyc
14	29	58.0	11	3	AAY69924	Aay69924 Human cyc
15	28	56.0	9	5	ABG94771	Abg94771 Replikin
16	28	56.0	9	5	ABG94772	Abg94772 Replikin
17	28	56.0	9	6	ABU57321	Abu57321 Replikin
18	28	56.0	9	6	ABU57322	Abu57322 Replikin
19	28	56.0	9	7	ADD88394	Add88394 Tumour vi
20	28	56.0	9	7	ADD88395	Add88395 Tumour vi
21	28	56.0	9	7	ADG18172	Adg18172 Tumour vi
22	28	56.0	9	7	ADG18173	Adg18173 Tumour vi
23	28	56.0	12	8	ADI46367	Adi46367 Permeabil
24	27	54.0	9	5	AAU71498	Aau71498 Human MHC
25	27	54.0	9	5	AAU71218	Aau71218 Human MHC
26	27	54.0	10	5	AAU71556	Aau71556 Human MHC
27	27	54.0	10	5	AAU71745	Aau71745 Human MHC
28	27	54.0	10	8	ADM41409	Adm41409 Human bet
29	27	54.0	12	2	AAW92359	Aaw92359 CYP2B1 im
30	26	52.0	11	2	AAR48203	Aar48203 Human pho
31	26	52.0	11	4	AAB82291	Aab82291 Phosphory
32	26	52.0	11	4	AAB82294	Aab82294 Phosphory
33	26	52.0	12	1	AAP93365	Aap93365 Amino aci
34	25.5	51.0	9	4	ABP11571	Abp11571 HIV A01 s
35	25.5	51.0	9	4	ABP15315	Abp15315 HIV A24 s
36	25.5	51.0	10	4	ABP20150	Abp20150 HIV A03 m
37	25.5	51.0	10	4	ABP15417	Abp15417 HIV A24 s
38	25.5	51.0	11	4	ABP11625	Abp11625 HIV A01 s
39	25.5	51.0	11	4	ABP15505	Abp15505 HIV A24 s
40	25.5	51.0	11	4	ABP20151	Abp20151 HIV A03 m
41	25.5	51.0	11	4	ABP17665	Abp17665 HIV B58 s
42	25.5	51.0	11	4	ABP15503	Abp15503 HIV A24 s
43	25	50.0	7	7	ADB79463	Adb79463 Parapoxvi
44	25	50.0	7	8	ADP74879	Adp74879 Parapoxvi
45	25	50.0	9	6	ABR11047	Abr11047 Human can

ALIGNMENTS

RESULT 1
AAY69962
ID AAY69962 standard; peptide; 9 AA.
XX
AC AAY69962;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #42.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHRVIKDF 9
|||||||||

```
Db          1 KYHRVIKDF 9


RESULT 2
AAB46946
ID   AAB46946 standard; peptide; 9 AA.
XX
AC   AAB46946;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 19; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 50;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |||||||||
Db          1 KYHRVIKDF 9


RESULT 3
AAY69921
ID   AAY69921 standard; peptide; 9 AA.
XX
AC   AAY69921;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #1.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 49; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             92.0%;  Score 46;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 4
AAB46930
ID   AAB46930 standard; peptide; 9 AA.
XX
AC   AAB46930;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
```

XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 15; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHRVIKDF 9
|:|||||||
Db 1 KFHRVIKDF 9

RESULT 5
AAG68088
ID AAG68088 standard; peptide; 9 AA.
XX
AC AAG68088;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 84-92.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHRVIKDF 9
|:|||||||
Db 1 KFHRVIKDF 9

RESULT 6
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following

```
CC   the administration, animal is protected from disease, where the animal
CC   comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC   disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC   cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC   cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC   breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC   The animal is further subjected to a cancer treatment including surgery,
CC   radiation, chemotherapy or gene therapy. The administration of (I),
CC   preferably dendritic cell is prior to, subsequent to or concurrent with,
CC   the cancer treatment. The present sequence is a tumour antigen derived
CC   epitope for inclusion in the composition of the invention
XX
SQ   Sequence 9 AA;

  Query Match             92.0%;  Score 46;  DB 5;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 7
ABR84373
ID   ABR84373 standard; peptide; 9 AA.
XX
AC   ABR84373;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human CypB HLA-A24 epitope, SEQ ID NO:23.
XX
KW   Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW   cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW   immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW   human; human leukocyte antigen; HLA-A24 epitope.
XX
OS   Homo sapiens.
XX
PN   JP2002365286-A.
XX
PD   18-DEC-2002.
XX
PF   18-SEP-2001; 2001JP-00283413.
XX
PR   13-NOV-2000; 2000JP-00345094.
XX
PA   (ITOY/) ITO Y.
XX
DR   WPI; 2003-508315/48.
XX
PT   A detection method of antigen specific T-cells, comprises the use of
PT   plural antigenic peptides, useful in semi-quantitative determination of
PT   cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS   Example 8; Page 10; 18pp; Japanese.
XX
CC   The invention relates to a method for the detection of antigen specific T
CC   -cells in a blood sample involving the use of a plurality of antigenic
CC   peptides. The method comprises sampling of peripheral blood monocytes;
CC   stimulation of the collected peripheral blood monocytes with antigens
CC   without direct use of antigen presenting cells; and detection of T-cells
CC   specific to the antigen in the stimulated monocytes. The method is
CC   particularly used for the detection of cancer as it can be used in semi-
CC   quantitative determination of cancer specific T-cells. It can also be
CC   used for cancer vaccine therapy for patients with cervical or prostate
CC   cancer. The method can additionally be used to monitor of cellular
CC   immunity and cancer immune therapy by detection of specific T-cell
CC   frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC   leukocyte antigen) peptides of human origin used in an example from the
CC   invention
XX
SQ   Sequence 9 AA;

  Query Match             92.0%;  Score 46;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 8
ADC17701
ID   ADC17701 standard; peptide; 9 AA.
XX
AC   ADC17701;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Cyclophilin B protein amino acids 84-92.
XX
KW   cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW   allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW   cyclophilin B.
XX
OS   Synthetic.
XX
PN   WO2003020306-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002WO-JP008641.
XX
PR   29-AUG-2001; 2001JP-00260046.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Yamada A;
XX
DR   WPI; 2003-300831/29.
XX
PT   Desensitizers or allergic reaction suppressors containing peptides
PT   originating from the same antigenic substances as reaction-inducing
PT   substances, useful for preventing or treating type I allergic diseases
PT   and in cancer vaccines.
XX
PS   Claim 8; SEQ ID NO 1; 49pp; Japanese.
XX
CC   The invention relates to allergic reaction suppressors, comprising a
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 84-92 of the cyclophilin B protein.
XX
SQ   Sequence 9 AA;

  Query Match             92.0%;  Score 46;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 9
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```
ADG89641
ID   ADG89641 standard; peptide; 9 AA.
XX
AC   ADG89641;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Class I HLA-restricted widely expressed antigen #6.
XX
KW   metastatic cancer cell differentiation; mutated fibronectin;
KW   metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS   Unidentified.
XX
PN   WO2003100027-A2.
XX
PD   04-DEC-2003.
XX
PF   28-MAY-2003; 2003WO-US016736.
XX
PR   28-MAY-2002; 2002US-0383530P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Wang R;
XX
DR   WPI; 2004-035134/03.
XX
PT   Identifying a cell that differentiates into a metastatic cancer cell,
PT   useful for preventing metastatic cancer, comprises identifying a mutated
PT   fibronectin in the cell.
XX
PS   Disclosure; SEQ ID NO 84; 137pp; English.
XX
CC   The invention comprises a method for identifying a cell that will
CC   differentiate into a metastatic cancer cell, the method involves
CC   identifying a mutated fibronectin in the cell. The method of the
CC   invention is useful for preventing metastatic cancer. The present amino
CC   acid sequence represents a Class I HLA-restricted widely expressed
CC   antigen.
XX
SQ   Sequence 9 AA;

  Query Match             92.0%;  Score 46;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 10
AAY69960
ID   AAY69960 standard; peptide; 9 AA.
XX
AC   AAY69960;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #40.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Tyr, Met, Trp
FT   Misc-difference 9
FT                   /label= Phe, Leu, Ile, Trp, Met
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 10; Page 59; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             72.0%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              | ||||||
Db          1 KXHRVIKD 8


RESULT 11
AAR96521
ID   AAR96521 standard; peptide; 10 AA.
XX
AC   AAR96521;
XX
DT   07-MAR-1997  (first entry)
XX
DE   Hepatitis C virus type 9 peptide.
XX
KW   Hepatitis C virus; subtype; polymerase chain reaction; amplification;
KW   PCR; primer; probe; antibody; infection.
XX
OS   Synthetic.
XX
PN   WO9613590-A2.
XX
PD   09-MAY-1996.
XX
PF   23-OCT-1995;   95WO-EP004155.
XX
PR   21-OCT-1994;   94EP-00870166.
PR   28-JUN-1995;   95EP-00870076.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Maertens G,  Stuyver L;
XX
DR   WPI; 1996-251460/25.
XX
PT   Hepatitis C virus poly:nucleic acid unique to unidentified sub:type -
PT   used to develop probes and primers for new sub:types and vaccines to
PT   prevent and treat infection.
XX
PS   Claim 5; Page 68; 150pp; English.
XX
CC   The peptides AAR96424-R96524 represent novel peptides derived from the
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CC   novel hepatitis C virus subtypes 1d-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-c or
CC   types 9, 10 or 11 (see AAT27937-T27989). The sequences corresp. to the 5'
CC   untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.
CC   This sequence is from the HCV subtype 9. The new HCV types were isolated
CC   from patients with chronic HCV from the Benelux countries, France,
CC   Cameroon and Vietnam, because of their aberrant reactivities. The RNA was
CC   extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The
CC   5'UR, Core/E1 and NS5B regions were sequenced either directly or
CC   partially and used to classify the new viruses into (sub)types based on
CC   comparison with known sequences. The nucleotide sequences can be used to
CC   synthesise probes and primers for the detection of HCV in a sample. The
CC   polypeptides can be used to detect anti-HCV antibodies, for HCV typing or
CC   to prevent HCV infections
XX
SQ   Sequence 10 AA;

  Query Match             62.0%;  Score 31;  DB 2;  Length 10;
  Best Local Similarity   62.5%;  Pred. No. 31;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              |||:| :|
Db          3 KYHQVTQD 10


RESULT 12
AAB82292
ID   AAB82292 standard; peptide; 11 AA.
XX
AC   AAB82292;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Phosphorylation site in potato HMG-CoA reductase.
XX
KW   3-Hydroxy-3-methylglutaryl-CoA reductase; HMG-CoA reductase; HMGR;
KW   phosphorylation; isoprenoid; sterol; transgenic plant; potato;
KW   pathogen resistance; disease resistance; crop protection.
XX
OS   Solanum tuberosum.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "O-phosphorylated"
XX
PN   WO200131043-A1.
XX
PD   03-MAY-2001.
XX
PF   27-OCT-2000; 2000WO-GB004141.
XX
PR   27-OCT-1999;   99GB-00025453.
XX
PA   (UYBR-) UNIV BRISTOL.
XX
PI   Halford NG,  Hey SJ,  Beale MH;
XX
DR   WPI; 2001-308654/32.
XX
PT   Modified 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, useful for
PT   generating transgenic plants having increased isoprenoid production,
PT   comprising a modified phosphorylation site.
XX
PS   Claim 16; Page 18; 23pp; English.
XX
CC   The present sequence is that of a phosphorylated region of the 3-hydroxy-
CC   3-methylglutaryl-coenzyme A reductase (HMGR) protein of potato. The
CC   invention relates to modified HMGR genes useful for generating transgenic
CC   plants having increased isoprenoid (especially sterol) production. The
CC   modified genes encode modified HMGR proteins, in which a phosphorylation
CC   site has been rendered inactive by replacing a Ser, Thr or Tyr residue
CC   with Ala or other amino acid residue. This reduces transcriptional
CC   regulation. The HMGR genes may be in the form of mutant plant and
CC   plant/non-plant or different plant chimeric genes. Transcriptional
CC   regulation can also be avoided by using heterologous promoters. Increased
CC   seed sterol content has been demonstrated in transgenic plants. The
CC   invention is used to produce plants having increased insect and mite pest
CC   resistance, particularly against species of Homoptera, Diptera,
CC   Lepidoptera, Coleoptera, Hymenoptera, Hemiptera, Dictyoptera, Orthoptera,
CC   arachnids and mites, or it is used to attract beneficial insects,
CC   including Odonata, Hymenoptera, Coleoptera, Neuroptera, or arachnids or
CC   mites to the plant. It is also used to produce plants having increased
CC   pathogen resistance, particularly against a fungus, especially Fusarium,
CC   Aspergillus, Phytophthora, Gaeumannomyces, Downy mildews, Colletotrichum,
CC   Cochliobolus, Tapesia, Magnaporthe, Stagnospora, Rhynchosporium,
CC   Septoria, Helminthosporium, and powdery mildews such as Blumeria and
CC   Erysiphe. The modified genes are particularly useful in maize, wheat,
CC   rice, barley, oilseed rape, beans, sunflower, cabbage, potato, spinach,
CC   broccoli, pea, cauliflower, tomato, forest trees, roses and tea. The
CC   invention may also be used to add nutritional benefit such as fat-soluble
CC   vitamins E and K, and sterols to a crop plant
XX
SQ   Sequence 11 AA;

  Query Match             62.0%;  Score 31;  DB 4;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              ||:| |||
Db          3 KYNRSIKD 10


RESULT 13
AAY69959
ID   AAY69959 standard; peptide; 9 AA.
XX
AC   AAY69959;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #39.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 61; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             58.0%;  Score 29;  DB 3;  Length 9;
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  Best Local Similarity   62.5%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YHRVIKDF 9
              :|||| |
Db          2 FHRVIPSF 9
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```
RESULT 14
AAY69924
ID   AAY69924 standard; peptide; 11 AA.
XX
AC   AAY69924;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #4.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 50; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 11 AA;

  Query Match             58.0%;  Score 29;  DB 3;  Length 11;
  Best Local Similarity   83.3%;  Pred. No. 83;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVI 6
              |:||||
Db          6 KFHRVI 11
```

```
RESULT 15
ABG94771
ID   ABG94771 standard; peptide; 9 AA.
XX
AC   ABG94771;
XX
DT   02-DEC-2002  (first entry)
XX
DE   Replikin sequence identiied by the 3-point recognition method #44.
XX
KW   Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
KW   3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
KW   Surface Antigen S Precursor Protein.
XX
OS   Polyoma virus.
XX
PN   US2002120106-A1.
XX
PD   29-AUG-2002.
XX
PF   26-OCT-2001; 2001US-00984056.
XX
PR   04-SEP-1998;   98US-00146755.
PR   27-MAR-2001; 2001US-00817144.
PR   27-MAR-2001; 2001US-0278761P.
PR   09-JUL-2001; 2001US-0303396P.
XX
PA   (BOGO/) BOGOCH S.
PA   (BOGO/) BOGOCH E S.
XX
PI   Bogoch S,  Bogoch ES;
XX
DR   WPI; 2002-691212/74.
XX
PT   Isolated Bacillus anthracis and small pox virus peptides (I), also known
PT   as replikins, useful for formulating vaccines for treating anthrax or
PT   small pox, comprise 7 to 50 amino acids.
XX
PS   Disclosure; Page 3; 16pp; English.
XX
CC   The invention relates to isolated Bacillus anthracis and small pox virus
CC   peptides, also known as replikins, comprising 7 to 50 amino acids
CC   including at least one lysine residue located six to ten residues from a
CC   second lysine residue, at least one histidine residue, and at least 6%
CC   lysine residues. The peptides were identified using the 3-point-
CC   recognition method and based on the replikin sequence isolated from
CC   glioblastoma cells malignin peptide which is of non-human origin. Also
CC   included are anti-replikin antibodies (or antibody cocktail), a method of
CC   stimulating the immune system of a subject to produce antibodies to
CC   Bacillus anthracis or small pox comprising administering an effective
CC   amount of at least one or more Bacillus anthracis or small pox replikin
CC   and an antisense nucleic acid molecule complementary to a mRNA encoding a
CC   Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-
CC   107) comprising a replikin sequence, an antisense nucleic acid molecule
CC   complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.
CC   Surface Antigen S Precursor Protein comprising a replikin sequence. The
CC   peptides are useful for stimulating the immune system of a subject to
CC   produce antibodies that bind specifically to Anthrax or small pox
CC   polypeptides containing a replikin sequence. The peptides are useful for
CC   generating antibodies that can be used in the treatment and/or prevention
CC   of anthrax or small pox. The peptides are also useful for formulating
CC   vaccines for treating anthrax or small pox. The present sequence is a
CC   replikin sequence isolated by the 3-point-recognition system and sharing
CC   structural similarity with the replikin sequence isolated from
CC   glioblastoma cells malignin
XX
SQ   Sequence 9 AA;

  Query Match             56.0%;  Score 28;  DB 5;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
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Search completed: October 21, 2004, 07:21:03
Job time : 85 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	62.0	10	3	US-08-836-075A-204	Sequence 204, App
2	29	58.0	11	4	US-09-418-780A-14	Sequence 14, Appl
3	29	58.0	11	4	US-09-418-780A-22	Sequence 22, Appl
4	27	54.0	12	2	US-08-471-286-1	Sequence 1, Appli
5	25	50.0	11	1	US-08-503-062-8	Sequence 8, Appli
6	25	50.0	11	5	PCT-US96-11495-8	Sequence 8, Appli
7	25	50.0	12	2	US-08-973-563A-31	Sequence 31, Appl
8	25	50.0	12	2	US-08-973-559-31	Sequence 31, Appl
9	25	50.0	12	3	US-08-993-235-11	Sequence 11, Appl
10	25	50.0	12	4	US-09-226-666-7	Sequence 7, Appli
11	25	50.0	12	4	US-08-993-235-11	Sequence 11, Appl
12	25	50.0	12	4	US-10-037-311B-16	Sequence 16, Appl
13	24	48.0	11	1	US-08-378-761A-68	Sequence 68, Appl
14	24	48.0	11	1	US-08-485-286-68	Sequence 68, Appl
15	23	46.0	12	4	US-09-226-666-17	Sequence 17, Appl
16	23	46.0	12	5	PCT-US94-05905-10	Sequence 10, Appl
17	22	44.0	7	2	US-08-292-968-31	Sequence 31, Appl
18	22	44.0	7	2	US-08-467-974-31	Sequence 31, Appl
19	22	44.0	7	2	US-08-467-536-31	Sequence 31, Appl
20	22	44.0	7	3	US-08-467-976-31	Sequence 31, Appl
21	22	44.0	7	3	US-09-082-514-31	Sequence 31, Appl
22	22	44.0	8	4	US-09-535-852-1043	Sequence 1043, Ap
23	22	44.0	9	2	US-08-646-981-13	Sequence 13, Appl
24	22	44.0	9	4	US-09-417-608A-16	Sequence 16, Appl
25	22	44.0	9	4	US-09-417-608A-41	Sequence 41, Appl
26	22	44.0	10	2	US-08-556-597-122	Sequence 122, App
27	22	44.0	10	4	US-09-878-281A-264	Sequence 264, App
28	22	44.0	12	1	US-07-778-233B-29	Sequence 29, Appl
29	22	44.0	12	1	US-07-963-321-29	Sequence 29, Appl
30	22	44.0	12	1	US-08-290-641-29	Sequence 29, Appl
31	22	44.0	12	1	US-08-548-540-29	Sequence 29, Appl
32	22	44.0	12	3	US-08-742-243-6	Sequence 6, Appli
33	22	44.0	12	3	US-08-742-243-7	Sequence 7, Appli
34	22	44.0	12	3	US-08-742-243-8	Sequence 8, Appli
35	22	44.0	12	3	US-08-742-243-9	Sequence 9, Appli
36	22	44.0	12	5	PCT-US96-09809-29	Sequence 29, Appl
37	21	42.0	6	4	US-08-877-605-93	Sequence 93, Appl
38	21	42.0	6	4	US-08-877-605-94	Sequence 94, Appl
39	21	42.0	7	2	US-08-188-583-42	Sequence 42, Appl
40	21	42.0	7	2	US-08-292-968-37	Sequence 37, Appl
41	21	42.0	7	2	US-08-623-833B-45	Sequence 45, Appl
42	21	42.0	7	2	US-08-467-974-37	Sequence 37, Appl
43	21	42.0	7	2	US-08-467-536-37	Sequence 37, Appl
44	21	42.0	7	3	US-08-467-976-37	Sequence 37, Appl
45	21	42.0	7	3	US-09-082-514-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-836-075A-204
; Sequence 204, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-204

Query Match 62.0%; Score 31; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              |||:| :|
Db          3 KYHQVTQD 10


RESULT 2
US-09-418-780A-14
; Sequence 14, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/09/418,780A
;  CURRENT FILING DATE:  1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-418-780A-14

  Query Match             58.0%;  Score 29;  DB 4;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              ||::||
Db          1 YHKIIK 6


RESULT 3
US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/09/418,780A
;  CURRENT FILING DATE:  1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-418-780A-22

  Query Match             58.0%;  Score 29;  DB 4;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 27;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              ||::||
Db          1 YHKIIK 6


RESULT 4
US-08-471-286-1
; Sequence 1, Application US/08471286
; Patent No. 5866688
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Hyesook
;    APPLICANT:  Charnecki, Jonathan
;    APPLICANT:  Putt, David A.
;    APPLICANT:  Kim, Edward Y.
;    TITLE OF INVENTION:  PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
;    TITLE OF INVENTION:  AGAINST CYTOCHROME P450
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099-4390
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,286
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-301 (Oxford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-471-286-1

  Query Match             54.0%;  Score 27;  DB 2;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 70;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              ||| ||
Db          7 HRVTKD 12


RESULT 5
US-08-503-062-8
; Sequence 8, Application US/08503062
; Patent No. 5723300
;  GENERAL INFORMATION:
;    APPLICANT:  Denis, Gerald V.
;    APPLICANT:  Green, Michael R.
;    TITLE OF INVENTION:  NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
;    TITLE OF INVENTION:  KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,062
;      FILING DATE:  10-JUL-1995
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  04020/080001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-503-062-8

  Query Match             50.0%;  Score 25;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              || :||
Db          1 YHDIIK 6


RESULT 6
PCT-US96-11495-8
; Sequence 8, Application PC/TUS9611495
;  GENERAL INFORMATION:
;    APPLICANT:  UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
;    TITLE OF INVENTION:  NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
;    TITLE OF INVENTION:  KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/11495
;      FILING DATE:  03-JUL-1996
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/503,062
;      FILING DATE:  10-JUL-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  04020/080WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-11495-8

  Query Match             50.0%;  Score 25;  DB 5;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              || :||
Db          1 YHDIIK 6


RESULT 7
US-08-973-563A-31
; Sequence 31, Application US/08973563A
; Patent No. 5885965
;  GENERAL INFORMATION:
;    APPLICANT:  Oppenheim, Frank G.
;    APPLICANT:  Xu, Tao
;    APPLICANT:  Spacciapoli, Peter
;    APPLICANT:  Roberts, F. D.
;    APPLICANT:  Friden, Philip M.
;    TITLE OF INVENTION:  Anti-Fungal D-Amino Acid Histatin-Based
;    TITLE OF INVENTION:  Peptides
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/973,563A
;      FILING DATE:  07-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,273
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  PER95-02A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  781-861-6240
;      TELEFAX:  781-861-9540
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Region
;      LOCATION:  1..12
;      OTHER INFORMATION:  /note= "At least one amino acid
;      OTHER INFORMATION:  must have a D configuration."
US-08-973-563A-31

  Query Match             50.0%;  Score 25;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHR 4
              ||||
Db          6 KYHR 9


RESULT 8
US-08-973-559-31
; Sequence 31, Application US/08973559
; Patent No. 5912230
```

; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-559-31

Query Match 50.0%; Score 25; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
||||
Db 6 KYHR 9

RESULT 9
US-08-993-235-11
; Sequence 11, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-11

Query Match 50.0%; Score 25; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
||||
Db 6 KYHR 9

RESULT 10
US-09-226-666-7
; Sequence 7, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-7

Query Match 50.0%; Score 25; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
||||
Db 6 KYHR 9

RESULT 11
US-08-993-235-11
; Sequence 11, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-11

Query Match 50.0%; Score 25; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
||||
Db 6 KYHR 9

RESULT 12
US-10-037-311B-16

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; Sequence 16, Application US/10037311B
; Patent No. 6747190
; GENERAL INFORMATION:
;  APPLICANT: MICHIGAN STATE UNIVERSITY
;  TITLE OF INVENTION: XYLOGLUCAN FUCOSYLTRANSFERASES
;  FILE REFERENCE: MS00-001C2
;  CURRENT APPLICATION NUMBER: US/10/037,311B
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER: US60/117,555
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Cross-species
US-10-037-311B-16

  Query Match             50.0%;  Score 25;  DB 4;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |:||:|
Db          6 HQVIRD 11


RESULT 13
US-08-378-761A-68
; Sequence 68, Application US/08378761A
; Patent No. 5635384
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,761A
;      FILING DATE:  26-JAN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-761A-68

  Query Match             48.0%;  Score 24;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 2.3e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              |  ||:||
Db          3 KKARVVKD 10


RESULT 14
US-08-485-286-68
; Sequence 68, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
;  GENERAL INFORMATION:
;    APPLICANT:  WALSH, TERENCE A
;    APPLICANT:  HEY, TIMOTHY D
;    APPLICANT:  MORGAN, ALICE ER
;    TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
;    TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
;    TITLE OF INVENTION:  USING
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ANDREA T. BORUCKI
;      STREET:  9330 ZIONSVILLE ROAD
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  US
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,286
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/378761
;      FILING DATE:  26-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BORUCKI, ANDREA T
;      REGISTRATION NUMBER:  33651
;      REFERENCE/DOCKET NUMBER:  38272B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317) 337-4846
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-485-286-68

  Query Match             48.0%;  Score 24;  DB 1;  Length 11;
  Best Local Similarity   62.5%;  Pred. No. 2.3e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              |  ||:||
Db          3 KKARVVKD 10


RESULT 15
US-09-226-666-17
; Sequence 17, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
;  APPLICANT: Spacciapoli, Peter
;  APPLICANT: Rothstein, David M.
;  APPLICANT: Friden, Phillip M.
;  TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
;  FILE REFERENCE: 50032/007001
;  CURRENT APPLICATION NUMBER: US/09/226,666A
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;  CURRENT FILING DATE: 1999-01-08
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 12
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-17

  Query Match             46.0%;  Score 23;  DB 4;  Length 12;
  Best Local Similarity   44.4%;  Pred. No. 3.9e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|:  | |
Db          3 KHHKYHKKF 11


Search completed: October 21, 2004, 07:29:30
Job time : 22.5 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	92.0	9	15	US-10-447-161-84	Sequence 84, Appl
2	46	92.0	9	16	US-10-788-016-1	Sequence 1, Appli
3	31	62.0	10	9	US-09-851-138-204	Sequence 204, App
4	29	58.0	11	14	US-10-293-822-14	Sequence 14, Appl
5	29	58.0	11	14	US-10-293-822-22	Sequence 22, Appl
6	28	56.0	9	9	US-09-984-056-61	Sequence 61, Appl
7	28	56.0	9	9	US-09-984-056-62	Sequence 62, Appl
8	28	56.0	9	9	US-09-984-057-61	Sequence 61, Appl
9	28	56.0	9	9	US-09-984-057-62	Sequence 62, Appl
10	28	56.0	9	14	US-10-105-232-61	Sequence 61, Appl
11	28	56.0	9	14	US-10-105-232-62	Sequence 62, Appl
12	28	56.0	9	14	US-10-189-437-61	Sequence 61, Appl
13	28	56.0	9	14	US-10-189-437-62	Sequence 62, Appl
14	28	56.0	12	15	US-10-601-953-76	Sequence 76, Appl
15	27	54.0	9	9	US-09-834-765-139	Sequence 139, App
16	27	54.0	9	9	US-09-834-765-419	Sequence 419, App
17	27	54.0	10	9	US-09-834-765-477	Sequence 477, App
18	27	54.0	10	9	US-09-834-765-666	Sequence 666, App
19	25	50.0	10	10	US-09-572-270A-759	Sequence 759, App
20	25	50.0	12	9	US-09-226-666-7	Sequence 7, Appli
21	25	50.0	12	15	US-10-601-953-64	Sequence 64, Appl
22	24	48.0	7	14	US-10-191-540-182	Sequence 182, App
23	24	48.0	9	14	US-10-211-207-23	Sequence 23, Appl
24	24	48.0	9	14	US-10-211-207-24	Sequence 24, Appl
25	24	48.0	9	14	US-10-077-106-23	Sequence 23, Appl
26	24	48.0	9	14	US-10-077-106-24	Sequence 24, Appl
27	23	46.0	8	16	US-10-712-425-1130	Sequence 1130, Ap
28	23	46.0	9	14	US-10-353-929-5	Sequence 5, Appli
29	23	46.0	11	9	US-09-984-056-72	Sequence 72, Appl
30	23	46.0	11	9	US-09-984-057-72	Sequence 72, Appl
31	23	46.0	11	14	US-10-105-232-72	Sequence 72, Appl
32	23	46.0	11	14	US-10-189-437-72	Sequence 72, Appl
33	23	46.0	12	9	US-09-226-666-17	Sequence 17, Appl
34	22	44.0	7	14	US-10-105-232-265	Sequence 265, App
35	22	44.0	7	14	US-10-405-339-26	Sequence 26, Appl
36	22	44.0	7	14	US-10-405-339-39	Sequence 39, Appl
37	22	44.0	7	14	US-10-405-339-42	Sequence 42, Appl
38	22	44.0	7	14	US-10-189-437-252	Sequence 252, App
39	22	44.0	9	16	US-10-730-454-16	Sequence 16, Appl
40	22	44.0	9	16	US-10-730-454-41	Sequence 41, Appl
41	22	44.0	10	9	US-09-819-308-29	Sequence 29, Appl
42	22	44.0	10	10	US-09-899-046-264	Sequence 264, App
43	22	44.0	10	10	US-09-878-281-264	Sequence 264, App
44	22	44.0	10	10	US-09-873-224-264	Sequence 264, App
45	22	44.0	11	9	US-09-795-006A-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 92.0%; Score 46; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHRVIKDF 9
|:|||||||
Db 1 KFHRVIKDF 9

RESULT 2
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo

```
;  TITLE OF INVENTION: Desensitizers
;  FILE REFERENCE: 3190-049
;  CURRENT APPLICATION NUMBER: US/10/788,016
;  CURRENT FILING DATE:  2004-02-26
;  PRIOR APPLICATION NUMBER: PCT/JP02/08641
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: JP P2001-260046
;  PRIOR FILING DATE: 2001-08-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
;   OTHER INFORMATION: to the 92nd residue of cyclophillin B
US-10-788-016-1

  Query Match             92.0%;  Score 46;  DB 16;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKDF 9
              |:|||||||
Db          1 KFHRVIKDF 9


RESULT 3
US-09-851-138-204
; Sequence 204, Application US/09851138
; Publication No. US20020183508A1
;  GENERAL INFORMATION:
;       APPLICANT: MAERTENS, GEERT
;                  STUYVER, LIEVEN
;       TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
;                           AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
;                           AGENTS
;       NUMBER OF SEQUENCES: 207
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: ARNOLD, WHITE & DURKEE
;            STREET: P.O. BOX 4433
;            CITY: HOUSTON
;            STATE: TEXAS
;            COUNTRY: USA
;            ZIP: 77210-4433
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Microsoft Word 6.0 / ASCII text output
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/851,138
;            FILING DATE: 09-May-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/836,075
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: EP 94870166.9
;            FILING DATE: 21 Oct 1994
;            APPLICATION NUMBER: EP 95870076.7
;            FILING DATE: 28 Jun 1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: KAMMERER, PATRICIA A.
;            REGISTRATION NUMBER: 29,775
;            REFERENCE/DOCKET NUMBER: INNS:004
;   INFORMATION FOR SEQ ID NO: 204:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204

  Query Match             62.0%;  Score 31;  DB 9;  Length 10;
  Best Local Similarity   62.5%;  Pred. No. 24;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              |||:| :|
Db          3 KYHQVTQD 10


RESULT 4
US-10-293-822-14
; Sequence 14, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/10/293,822
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: US/09/418,780
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-822-14

  Query Match             58.0%;  Score 29;  DB 14;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 64;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              ||::||
Db          1 YHKIIK 6


RESULT 5
US-10-293-822-22
; Sequence 22, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
;  APPLICANT: Jones, Michael H.
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
;  FILE REFERENCE: 06501-043001
;  CURRENT APPLICATION NUMBER: US/10/293,822
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: US/09/418,780
;  PRIOR FILING DATE: 1999-10-15
;  PRIOR APPLICATION NUMBER: PCT/JP98/01782
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: JAPAN 9/116402
;  PRIOR FILING DATE: 1997-04-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-293-822-22

  Query Match             58.0%;  Score 29;  DB 14;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 64;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              ||::||
```

```
Db          1 YHKIIK 6


RESULT 6
US-09-984-056-61
; Sequence 61, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
;  FILE REFERENCE: 09425-46903
;  CURRENT APPLICATION NUMBER: US/09/984,056
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-09-984-056-61

  Query Match           56.0%;  Score 28;  DB 9;  Length 9;
  Best Local Similarity  62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 7
US-09-984-056-62
; Sequence 62, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLIKINS AND METHODS OF USE
;  FILE REFERENCE: 09425-46903
;  CURRENT APPLICATION NUMBER: US/09/984,056
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-09-984-056-62

  Query Match           56.0%;  Score 28;  DB 9;  Length 9;
  Best Local Similarity  62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 8
US-09-984-057-61
; Sequence 61, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING
;  TITLE OF INVENTION:  REPLIKIN-CONTAINING SEQUENCES
;  FILE REFERENCE: 09425-46902
;  CURRENT APPLICATION NUMBER: US/09/984,057
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
US-09-984-057-61

  Query Match           56.0%;  Score 28;  DB 9;  Length 9;
  Best Local Similarity  62.5%;  Pred. No. 1.2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8


RESULT 9
US-09-984-057-62
; Sequence 62, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
;  APPLICANT: BOGOCH, SAMUEL
;  APPLICANT:  BOGOCH, ELENORE S.
;  TITLE OF INVENTION: REPLIKINS AND METHODS OF IDENTIFYING
;  TITLE OF INVENTION:  REPLIKIN-CONTAINING SEQUENCES
;  FILE REFERENCE: 09425-46902
;  CURRENT APPLICATION NUMBER: US/09/984,057
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: 60/303,396
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: 60/278,761
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/146,755
;  PRIOR FILING DATE: 1998-09-04
;  PRIOR APPLICATION NUMBER: 09/817,144
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 08/198,139
;  PRIOR FILING DATE: 1994-02-17
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Polyoma virus
```

US-09-984-057-62

Query Match 56.0%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 10
US-10-105-232-61
; Sequence 61, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-61

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 11
US-10-105-232-62
; Sequence 62, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-62

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 12
US-10-189-437-61
; Sequence 61, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-61

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              | || :||
Db          1 KQHRELKD 8
```

RESULT 13
US-10-189-437-62
; Sequence 62, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1

; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-62

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKD 8
              | ||  :||
Db          1 KQHRELKD 8
```

RESULT 14
US-10-601-953-76
; Sequence 76, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-76

Query Match 56.0%; Score 28; DB 15; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 HRVIKDF 9
              | :|:||
Db          1 HNIIQDF 7
```

RESULT 15
US-09-834-765-139
; Sequence 139, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-139

Query Match 54.0%; Score 27; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 YHRVIKDF 9
              |  |||:|
Db          1 YEHVIKNF 8
```

Search completed: October 21, 2004, 07:33:43
Job time : 62.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	40.0	10	2	S36849	Ig heavy chain V r
2	19	38.0	12	2	PC4377	telomeric and tetr
3	18	36.0	11	2	I54193	Rhesus blood group
4	17	34.0	10	2	PC4374	telomeric and tetr
5	17	34.0	10	2	JQ0943	hypothetical 1.3K
6	16	32.0	8	2	S65381	cytochrome-c oxida
7	16	32.0	10	2	B39308	glycine reductase
8	16	32.0	11	2	S23373	T-cell receptor al
9	16	32.0	12	2	G64003	hypothetical prote
10	15	30.0	7	1	NYPG7	hypothalamic hepta
11	15	30.0	10	2	S13224	virG protein - Agr
12	15	30.0	10	2	A59272	peptide-N4-(N-acet
13	15	30.0	11	2	PC2330	cycloinulooligosac
14	15	30.0	11	4	I52708	ELAV-like neuronal
15	15	30.0	12	2	S10624	lipovitellin - Afr
16	15	30.0	12	2	PT0228	Ig heavy chain CDR
17	15	30.0	12	2	PQ0730	unidentified 5.4/3
18	14	28.0	6	2	B44510	hypothetical prote
19	14	28.0	7	2	PT0246	Ig heavy chain CRD
20	14	28.0	8	2	S66296	Na+-transporting A
21	14	28.0	9	2	C36730	hutU protein - Kle
22	14	28.0	9	2	S78420	ribosomal protein
23	14	28.0	9	2	A44787	calliFMRFamide 10
24	14	28.0	9	2	I49406	bone gla protein -
25	14	28.0	10	2	B56899	serum heterodimer,
26	14	28.0	11	2	G42762	proteasome endopep
27	14	28.0	11	2	PQ0733	unidentified 6.0/1
28	14	28.0	11	2	PH1376	T antigen variant
29	14	28.0	11	2	PN0042	stathmin - mouse (
30	14	28.0	12	2	S09082	proteasome chain 1
31	14	28.0	12	2	S34447	binR protein - Sta
32	13	26.0	6	2	S02617	alcohol dehydrogen
33	13	26.0	6	2	B56979	collagen alpha 1(I
34	13	26.0	8	2	S69165	ferredoxin a2 - Ja
35	13	26.0	9	2	T31612	hypothetical prote
36	13	26.0	9	2	PT0315	Ig heavy chain CRD
37	13	26.0	9	2	A42266	peptidylglycine mo
38	13	26.0	9	2	D57444	neuropeptide Grb-A
39	13	26.0	9	2	A41978	calliFMRFamide 1 -
40	13	26.0	9	2	B41978	calliFMRFamide 2 -
41	13	26.0	9	2	C41978	calliFMRFamide 3 -
42	13	26.0	9	2	D41978	calliFMRFamide 4 -
43	13	26.0	9	2	E41978	calliFMRFamide 5 -
44	13	26.0	9	2	F41978	calliFMRFamide 6 -
45	13	26.0	9	2	G41978	calliFMRFamide 7 -

ALIGNMENTS

RESULT 1
S36849
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C;Accession: S36849
R;Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny]
A;Reference number: S25024
A;Accession: S36849
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-10 <JAC>
A;Cross-references: EMBL:X67382; NID:g50070; PIDN:CAA47794.1; PID:e51590; PID:g1333861
C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 20; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 KYHRVIKDF 9
              :|  |: :|
Db          2 RYRTVVVNF 10
```

RESULT 2
PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: PC4377
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA1
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4377
A;Molecule type: protein
A;Residues: 1-12 <SAR>
A;Cross-references: UNIPROT:Q9QX80; UNIPROT:Q9Z0U8; UNIPROT:O88311; UNIPROT:Q9QX81
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 38.0%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 KYHRV 5
              |:|  |
Db          3 KFHTV 7
```

RESULT 3

```
I54193
Rhesus blood group CcEe protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I54193
R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.
Genomics 19, 68-74, 1994
A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens
A;Reference number: I54193; MUID:94245182; PMID:8188244
A;Accession: I54193
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: UNIPROT:Q9UPC8; UNIPROT:Q99906; UNIPROT:Q9UK19; UNIPROT:Q9UPN0; UNIP
PROT:Q9UEC7; GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761
C;Genetics:
A;Gene: GDB:RHCE
A;Cross-references: GDB:229957; OMIM:111700
A;Map position: 1p36.2-1p34

  Query Match             36.0%;  Score 18;  DB 2;  Length 11;
  Best Local Similarity   42.9%;  Pred. No. 2.4e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KYHRVIK 7
              || | ::
Db          4 KYPRSVR 10


RESULT 4
PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C;Accession: PC4374
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4374
A;Molecule type: protein
A;Residues: 1-10 <SAR>
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

  Query Match             34.0%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KYHRV 5
              | ||:
Db          6 KEHRL 10


RESULT 5
JQ0943
hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)
C;Species: infectious bursal disease virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JQ0943
R;Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bours
J. Gen. Virol. 71, 1303-1312, 1990
A;Title: A comparison of the sequences of segment A of four infectious bursal disease vi
A;Reference number: JQ0941; MUID:90278420; PMID:2161902
A;Accession: JQ0943
A;Status: translation not shown
A;Molecule type: genomic RNA
A;Residues: 1-10 <BAY>
A;Cross-references: UNIPROT:Q82625; GB:D00869; NID:g221038; PIDN:BAA00743.1; PID:d100120

  Query Match             34.0%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.4e+03;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYH 3
              :||
Db          8 RYH 10


RESULT 6
S65381
cytochrome-c oxidase (EC 1.9.3.1) chain VIb, hepatic - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65381
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termi
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65381
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <SCH>
A;Cross-references: UNIPROT:P80430
C;Keywords: oxidoreductase

  Query Match             32.0%;  Score 16;  DB 2;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHR 4
              :||
Db          6 FHR 8


RESULT 7
B39308
glycine reductase (EC 1.4.99.-) sulfhydryl protein C, beta chain - Clostridium sticklandi
C;Species: Clostridium sticklandii
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C;Accession: B39308
R;Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A;Title: Glycine reductase protein C. Properties and characterization of its role in the
A;Reference number: A39308; MUID:92042141; PMID:1939235
A;Accession: B39308
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <STA>
A;Cross-references: UNIPROT:Q9EV92
C;Function:
A;Description: glycine reductase complex catalyzes the reductive deamination of glycine t
C;Keywords: ATP; oxidoreductase

  Query Match             32.0%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 5.3e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              ::|| |
Db          4 NKVIAD 9


RESULT 8
S23373
T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S23373
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmann
Eur. J. Immunol. 21, 2749-2754, 1991
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheun
A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23373
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-11 <PLU>
```

```
A;Cross-references: EMBL:X58168
C;Keywords: T-cell receptor

  Query Match             32.0%;  Score 16;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 5.9e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVI 6
              | :||
Db          6 YDKVI 10


RESULT 9
G64003
hypothetical protein HI0195 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C;Accession: G64003
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64003
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <TIGR>
A;Cross-references: GB:U32704; GB:L42023; NID:g1573143; PID:g1573155; TIGR:HI0195

  Query Match             32.0%;  Score 16;  DB 2;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 6.4e+03;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYH 3
              :||
Db          4 QYH 6


RESULT 10
NYPG7
hypothalamic heptapeptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong,
Horm. Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releasi
A;Reference number: A01417; MUID:81213980; PMID:6263778
A;Accession: A01417
A;Molecule type: protein
A;Residues: 1-7 <CHA>
A;Cross-references: UNIPROT:P01153
C;Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus

  Query Match             30.0%;  Score 15;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YH 3
              ||
Db          3 YH 4


RESULT 11
S13224
virG protein - Agrobacterium sp. (fragment)
C;Species: Agrobacterium sp.
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S13224
R;Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.
J. Mol. Biol. 215, 537-547, 1990
A;Title: Binding of the regulatory protein VirG to the phased signal sequences upstream f
A;Reference number: S13224; MUID:91039316; PMID:2231718
A;Accession: S13224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAM>
A;Cross-references: UNIPROT:Q7M0P7

  Query Match             30.0%;  Score 15;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 8.3e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KYHRVIKD 8
              |:  || |
Db          2 KHVLVIDD 9


RESULT 12
A59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain -
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: A59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
A;Cross-references: UNIPROT:P81899
C;Keywords: hydrolase

  Query Match             30.0%;  Score 15;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+03;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YH 3
              ||
Db          5 YH 6


RESULT 13
PC2330
cycloinulooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-255
C;Species: Bacillus circulans
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: PC2330
R;Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A;Title: Purification and characterization of cycloinulooligosaccharide fructanotransfera
A;Reference number: PC2330; MUID:95201377; PMID:7765973
A;Accession: PC2330
A;Molecule type: protein
A;Residues: 1-11 <KUS>
A;Cross-references: UNIPROT:Q7M0L3
C;Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecul
C;Keywords: glycosyltransferase; hexosyltransferase

  Query Match             30.0%;  Score 15;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+03;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YH 3
              ||
Db          1 YH 2


RESULT 14
I52708
```

ELAV-like neuronal protein 1, truncated splice form - human
N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: I52708
R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis
A;Reference number: I52708; MUID:94349312; PMID:8069866
A;Accession: I52708
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-11 <SEK>
A;Cross-references: UNIPROT:Q16234; GB:S73887; NID:g688242; PIDN:AAD14142.1; PID:g426184
C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
C;Genetics:
A;Gene: GDB:ELAVL4; HUD; PNEM
A;Cross-references: GDB:141875; OMIM:168360
A;Map position: 1p36-1p36
C;Keywords: alternative splicing

  Query Match 30.0%; Score 15; DB 4; Length 11;
  Best Local Similarity 50.0%; Pred. No. 9.1e+03;
  Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RVIK 7
   |::|
Db 6 RILK 9

RESULT 15
S10624
lipovitellin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S10624
R;Wallace, R.A.; Hoch, K.L.; Carnevali, O.
J. Mol. Biol. 213, 407-409, 1990
A;Title: Placement of small lipovitellin subunits within the vitellogenin precursor in X
A;Reference number: S10624; MUID:90278951; PMID:2352275
A;Accession: S10624
A;Molecule type: protein
A;Residues: 1-12 <WAL>

  Query Match 30.0%; Score 15; DB 2; Length 12;
  Best Local Similarity 42.9%; Pred. No. 1e+04;
  Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KYHRVIK 7
   |: | |
Db 1 KFQRPYK 7

Search completed: October 21, 2004, 07:27:59
Job time : 16.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	44.0	9	2	Q7SCD2	Q7scd2 neurospora
2	21	42.0	8	2	Q8AWV7	Q8awv7 anas platyr
3	21	42.0	8	2	Q8AWV8	Q8awv8 cygnus colu
4	21	42.0	8	2	Q8AWV9	Q8awv9 anser caeru
5	21	42.0	8	2	Q8AWW0	Q8aww0 coscoroba c
6	21	42.0	11	2	Q9XSP2	Q9xsp2 hylobates s
7	21	42.0	11	2	Q9XSP5	Q9xsp5 pan troglod
8	21	42.0	11	2	Q9XSP6	Q9xsp6 pongo pygma
9	21	42.0	11	2	Q9XSP7	Q9xsp7 pygathrix n
10	21	42.0	11	2	Q9XSP8	Q9xsp8 presbytis j
11	21	42.0	11	2	Q9XSQ4	Q9xsq4 gorilla gor
12	20	40.0	8	2	Q05403	Q05403 saccharomyc
13	20	40.0	10	2	Q9TQV4	Q9tqv4 e equus cab
14	20	40.0	12	2	Q9TT29	Q9tt29 saguinus oe
15	20	40.0	12	2	Q9TT31	Q9tt31 callithrix
16	19	38.0	10	2	Q8N6B1	Q8n6b1 homo sapien
17	18	36.0	12	2	Q7RGL4	Q7rgl4 plasmodium
18	17	34.0	9	1	BS43_SERPL	P83375 serratia pl
19	17	34.0	9	2	Q9TWX7	Q9twx7 manduca sex
20	17	34.0	9	2	Q8MJN1	Q8mjn1 cebuella py
21	17	34.0	9	2	Q8MJN2	Q8mjn2 callithrix
22	17	34.0	9	2	Q8MJN3	Q8mjn3 callimico g
23	17	34.0	9	2	Q8MJN4	Q8mjn4 leontopithe
24	17	34.0	9	2	Q8MJN5	Q8mjn5 saguinus fu
25	17	34.0	9	2	Q8MJN6	Q8mjn6 aotus azara
26	17	34.0	9	2	Q8MJN7	Q8mjn7 saimiri sci
27	17	34.0	9	2	Q8MJN8	Q8mjn8 cebus apell
28	17	34.0	9	2	Q8MJN9	Q8mjn9 ateles fusc
29	17	34.0	10	2	Q93LX4	Q93lx4 vibrio chol
30	17	34.0	10	2	Q8RJF1	Q8rjf1 pseudomonas
31	17	34.0	10	2	Q82625	Q82625 avian infec
32	17	34.0	11	2	Q8MEL7	Q8mel7 sida hooker
33	17	34.0	11	2	Q8MEL9	Q8mel9 pavonia has
34	17	34.0	11	2	Q8MEM2	Q8mem2 lagunaria p
35	17	34.0	11	2	Q8MEP0	Q8mep0 hibiscus pe
36	17	34.0	11	2	Q8MEP3	Q8mep3 hibiscus no
37	17	34.0	11	2	Q8MEP5	Q8mep5 hibiscus mi
38	17	34.0	11	2	Q8MEQ7	Q8meq7 hibiscus dr
39	17	34.0	11	2	Q8MER0	Q8mer0 hibiscus co
40	17	34.0	11	2	Q8MER1	Q8mer1 hibiscus ca
41	17	34.0	11	2	Q8MER7	Q8mer7 fioria viti
42	17	34.0	11	2	Q8MER8	Q8mer8 dombeya til
43	17	34.0	11	2	Q8MES1	Q8mes1 alyogyne pi
44	17	34.0	11	2	Q8MES3	Q8mes3 alyogyne cr
45	17	34.0	11	2	Q8MES5	Q8mes5 abelmoschus

ALIGNMENTS

RESULT 1
Q7SCD2
ID Q7SCD2 PRELIMINARY; PRT; 9 AA.
AC Q7SCD2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU05334.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000130; EAA34319.1; -.
SQ SEQUENCE 9 AA; 1173 MW; C483A32B50440449 CRC64;

Query Match 44.0%; Score 22; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.8e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 YHRVIKD 8
              ::|: ||
Db          2 FNRIYKD 8
```

RESULT 2
Q8AWV7
ID Q8AWV7 PRELIMINARY; PRT; 8 AA.
AC Q8AWV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123327; AAM96901.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 3
Q8AWV8
ID   Q8AWV8      PRELIMINARY;      PRT;     8 AA.
AC   Q8AWV8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Cygnus columbianus (tundra swan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
OX   NCBI_TaxID=110926;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123326; AAM96900.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 4
Q8AWV9
ID   Q8AWV9      PRELIMINARY;      PRT;     8 AA.
AC   Q8AWV9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Anser caerulescens caerulescens (snow goose).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX   NCBI_TaxID=70340;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123325; AAM96899.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 5
Q8AWW0
ID   Q8AWW0      PRELIMINARY;      PRT;     8 AA.
AC   Q8AWW0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   LDH-B (Fragment).
GN   Name=LDH-B;
OS   Coscoroba coscoroba (Coscoroba swan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
OX   NCBI_TaxID=8863;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cotter J.-P., StJohn J., Quinn T.W.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY123324; AAM96898.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  911 MW;  D73AADC2C05331F1 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 1.8e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIKD 8
              |::: |
Db          2 HKIVAD 7


RESULT 6
Q9XSP2
ID   Q9XSP2      PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9590;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243280; CAB45927.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
```

```
              :|| :|
Db          6 HHRSVK 11


RESULT 7
Q9XSP5
ID   Q9XSP5       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243277; CAB45926.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1331 MW;  7FB881F101E1F2D4 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              :|| :|
Db          6 HHRSVK 11


RESULT 8
Q9XSP6
ID   Q9XSP6       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243279; CAB45925.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              :|| :|
Db          6 HHRSVK 11


RESULT 9
Q9XSP7
ID   Q9XSP7       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Pygathrix nemaeus (Dove langur).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=54133;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243282; CAB45924.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              :|| :|
Db          6 HHRSVK 11


RESULT 10
Q9XSP8
ID   Q9XSP8       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSP8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
GN   Name=PDGFA;
OS   Presbytis johnii.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Presbytis.
OX   NCBI_TaxID=98375;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243281; CAB46013.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1345 MW;  7FB881F101E1E044 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              :|| :|
Db          6 HHRSVK 11


RESULT 11
Q9XSQ4
ID   Q9XSQ4       PRELIMINARY;      PRT;    11 AA.
AC   Q9XSQ4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Platelet-derived growth factor A chain (Fragment).
```

```
GN   Name=PDGFA;
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20065871; PubMed=10598812;
RA   Bonthron D.T., Smith S.L., Campbell R.;
RT   "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL   Hum. Genet. 105:452-459(1999).
DR   EMBL; AJ243278; CAB45916.1; -.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1331 MW;  7FB881F101E1F2D4 CRC64;

  Query Match             42.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YHRVIK 7
              :|| :|
Db          6 HHRSVK 11


RESULT 12
Q05403
ID   Q05403      PRELIMINARY;      PRT;     8 AA.
AC   Q05403;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Orf 00915 protein (Fragment).
GN   Name=orf 00915;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FY1679;
RX   MEDLINE=96021609; PubMed=8533473;
RA   Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT   "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT   more than twice as many unknown open reading frames.";
RL   Yeast 11:975-986(1995).
DR   EMBL; X83121; CAA58183.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  879 MW;  7B5322D2C441E058 CRC64;

  Query Match             40.0%;  Score 20;  DB 2;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HRVIK 7
              | |:|
Db          3 HNVVK 7


RESULT 13
Q9TQV4
ID   Q9TQV4      PRELIMINARY;      PRT;    10 AA.
AC   Q9TQV4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Equus caballus pop-variant * transferrin (Equus caballus clone 7
DE   transferrin) (Equus caballus pop-variant F1 transferrin) (Equus
DE   caballus pop-variant F2 transferrin) (Equus caballus pop-variant D
DE   transferrin) (Equus caballus pop-variant H2 transferrin) (Equus
DE   caballus pop-variant O transferrin) (Equus caballus pop-variant F3
DE   transferrin) (Equus caballus pop-variant G transferrin)
DE   (Fragment).
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Giffard J.M., Brandon R.B., Bell T.K.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF185778; AAF05491.1; -.
DR   EMBL; AF185770; AAF05483.1; -.
DR   EMBL; AF185771; AAF05484.1; -.
DR   EMBL; AF185772; AAF05485.1; -.
DR   EMBL; AF185773; AAF05486.1; -.
DR   EMBL; AF185774; AAF05487.1; -.
DR   EMBL; AF185775; AAF05488.1; -.
DR   EMBL; AF185776; AAF05489.1; -.
DR   EMBL; AF185777; AAF05490.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1188 MW;  6DF67DE9D1AEBDDB CRC64;

  Query Match             40.0%;  Score 20;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 5.5e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YHRV 5
              :|||
Db          7 FHRV 10


RESULT 14
Q9TT29
ID   Q9TT29      PRELIMINARY;      PRT;    12 AA.
AC   Q9TT29;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Beta-globin (Fragment).
OS   Saguinus oedipus (Cotton-top tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX   NCBI_TaxID=9490;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=20188801; PubMed=10723742;
RA   Francino M.P., Ochman H.;
RT   "Strand symmetry around the beta-globin origin of replication in
RT   primates.";
RL   Mol. Biol. Evol. 17:416-422(2000).
DR   EMBL; AF205415; AAF23766.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1251 MW;  07BC8AFAE8D72DD4 CRC64;

  Query Match             40.0%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYH 3
              |||
Db         10 KYH 12


RESULT 15
Q9TT31
ID   Q9TT31      PRELIMINARY;      PRT;    12 AA.
AC   Q9TT31;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Beta-globin (Fragment).
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
```

```
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=20188801; PubMed=10723742;
RA   Francino M.P., Ochman H.;
RT   "Strand symmetry around the beta-globin origin of replication in
RT   primates.";
RL   Mol. Biol. Evol. 17:416-422(2000).
DR   EMBL; AF205413; AAF23764.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1251 MW;  07BC8AFAE8D72DD4 CRC64;

  Query Match             40.0%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KYH 3
              |||
Db         10 KYH 12


Search completed: October 21, 2004, 07:26:50
Job time : 87 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	9	3	AAY69963	Aay69963 Human cyc
2	51	100.0	9	4	AAB46947	Aab46947 Human cyc
3	51	100.0	9	7	ADC17709	Adc17709 Modified
4	47	92.2	9	3	AAY69922	Aay69922 Human cyc
5	47	92.2	9	4	AAB46931	Aab46931 Human cyc
6	47	92.2	9	4	AAG68089	Aag68089 Antitumou
7	47	92.2	9	5	ABG79076	Abg79076 Human Cyp
8	47	92.2	9	6	ABR84374	Abr84374 Human Cyp
9	47	92.2	9	7	ADC17702	Adc17702 Cyclophil
10	47	92.2	9	8	ADG89642	Adg89642 Class I H
11	41	80.4	9	3	AAY69958	Aay69958 Human cyc
12	37	72.5	9	3	AAY69961	Aay69961 Human cyc
13	36	70.6	9	3	AAY69957	Aay69957 Human cyc
14	27.5	53.9	12	2	AAR91898	Aar91898 KGF-b min
15	27	52.9	9	2	AAR45361	Aar45361 Choline o
16	27	52.9	9	6	ABR16438	Abr16438 Human can
17	27	52.9	9	6	ABR16847	Abr16847 Human can
18	27	52.9	9	6	ABR16768	Abr16768 Human can
19	27	52.9	9	6	ABR16188	Abr16188 Human can
20	27	52.9	9	6	ABR16609	Abr16609 Human can
21	27	52.9	10	6	ABR17313	Abr17313 Human can
22	27	52.9	10	6	ABR16875	Abr16875 Human can
23	27	52.9	10	6	ABR16266	Abr16266 Human can
24	27	52.9	10	6	ABR16954	Abr16954 Human can
25	27	52.9	10	6	ABR16696	Abr16696 Human can
26	27	52.9	10	6	ABR16761	Abr16761 Human can
27	27	52.9	10	6	ABR16123	Abr16123 Human can
28	27	52.9	10	6	ABR16487	Abr16487 Human can
29	27	52.9	10	6	ABR17152	Abr17152 Human can
30	27	52.9	10	6	ABR16466	Abr16466 Human can
31	27	52.9	10	6	ABR16141	Abr16141 Human can
32	27	52.9	10	6	ABR16299	Abr16299 Human can
33	27	52.9	10	6	ABR16898	Abr16898 Human can
34	26	51.0	9	2	AAR72938	Aar72938 E. coli P
35	26	51.0	9	2	AAR72894	Aar72894 E. coli P
36	26	51.0	9	8	ADP49294	Adp49294 Natriuret
37	26	51.0	9	8	ADP49297	Adp49297 Natriuret
38	26	51.0	10	2	AAR72949	Aar72949 E. coli P
39	26	51.0	10	2	AAR72905	Aar72905 E. coli P
40	26	51.0	10	4	AAM42948	Aam42948 Mycoplasm
41	26	51.0	12	2	AAW21441	Aaw21441 HSV glyco
42	26	51.0	12	6	AAO31067	Aao31067 Human F8
43	25	49.0	9	2	AAR20729	Aar20729 Pancreas-
44	25	49.0	9	3	AAY51905	Aay51905 Elastase
45	25	49.0	9	4	AAM22987	Aam22987 HIV pepti

ALIGNMENTS

RESULT 1
AAY69963
ID AAY69963 standard; peptide; 9 AA.
XX
AC AAY69963;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #43.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 60; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|||||||||

```
Db          1 DYMIQGGDF 9


RESULT 2
AAB46947
ID   AAB46947 standard; peptide; 9 AA.
XX
AC   AAB46947;
XX
DT   04-MAY-2001  (first entry)
XX
DE   Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.
XX
KW   Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW   virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW   viral infectious disease; cyclophilin B; human.
XX
OS   Homo sapiens.
XX
PN   EP1074267-A1.
XX
PD   07-FEB-2001.
XX
PF   24-JUL-2000; 2000EP-00306263.
XX
PR   22-JUL-1999;   99JP-00207687.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI   Takasu H,  Gotoh M,  Yamaoka T;
XX
DR   WPI; 2001-193144/20.
XX
PT   Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT   the manufacture of an agent for the induction of antigen-specific T
PT   cells.
XX
PS   Disclosure; Page 20; 25pp; English.
XX
CC   This invention describes the novel use of interferons (IFNs) or DNAs
CC   capable of expressing the interferons and/or antigenic proteins (AP),
CC   antigenic peptides derived from the proteins or DNAs capable of
CC   expressing the antigenic proteins or peptides, in the manufacture of an
CC   agent for induction of antigen-specific T cells. The products of the
CC   invention have virucide and cytostatic activity and can be used for gene
CC   therapy or as inducers of antigen-specific T cells. The action of
CC   interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC   T cell (CTL) by administering an antigenic peptide in an incomplete
CC   Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC   DNA encoding IFNs) are useful in the manufacture of a medicament for
CC   inducing antigen-specific T cells in an individual who has been
CC   administered with AP (or DNA encoding AP) or vice versa. The medicament
CC   is useful for the treatment or prophylaxis of a tumor or a viral
CC   infectious disease
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGDF 9
              |||||||||
Db          1 DYMIQGGDF 9


RESULT 3
ADC17709
ID   ADC17709 standard; peptide; 9 AA.
XX
AC   ADC17709;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Modified cyclophilin B protein amino acids 91-99.
XX
KW   cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW   allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW   cyclophilin B.
XX
OS   Synthetic.
XX
PN   WO2003020306-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002WO-JP008641.
XX
PR   29-AUG-2001; 2001JP-00260046.
XX
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Yamada A;
XX
DR   WPI; 2003-300831/29.
XX
PT   Desensitizers or allergic reaction suppressors containing peptides
PT   originating from the same antigenic substances as reaction-inducing
PT   substances, useful for preventing or treating type I allergic diseases
PT   and in cancer vaccines.
XX
PS   Claim 8; SEQ ID NO 9; 49pp; Japanese.
XX
CC   The invention relates to allergic reaction suppressors, comprising a
CC   peptide which originates from the same antigenic substance as the
CC   antigenic substance inducing the (peptide-originated) allergic reaction,
CC   and containing an epitope different from the epitope participating in the
CC   induction of the allergic reaction and yet dos not induce the allergic
CC   reaction. The desensitizers or allergic reaction suppressors are useful
CC   for treating and preventing type I allergic diseases and in cancer
CC   vaccines for preventing or treating cancer. The allergic reaction
CC   suppressors are also useful for suppressing an allergic reaction or
CC   reducing immunoglobulin E antibody production, and for desensitization to
CC   antigens. This sequence represents a peptide used in the invention and
CC   corresponds to amino acids 91-99 of the cyclophilin B protein with the
CC   Phe at position 92 replaced by a Tyr.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGDF 9
              |||||||||
Db          1 DYMIQGGDF 9


RESULT 4
AAY69922
ID   AAY69922 standard; peptide; 9 AA.
XX
AC   AAY69922;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #2.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
```

XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 49; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 92.2%; Score 47; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 5
AAB46931
ID AAB46931 standard; peptide; 9 AA.
XX
AC AAB46931;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 15; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;

Query Match 92.2%; Score 47; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 6
AAG68089
ID AAG68089 standard; peptide; 9 AA.
XX
AC AAG68089;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 91-99.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,
CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;

```
  Query Match             92.2%;  Score 47;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGDF 9
              |:|||||||
Db          1 DFMIQGGDF 9
```

```
RESULT 7
ABG79076
ID   ABG79076 standard; peptide; 9 AA.
XX
AC   ABG79076;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human Cyp-B class I HLA widely expressed antigen peptide #2.
XX
KW   Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW   lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW   Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW   kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW   ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW   tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW   cytostatic; human.
XX
OS   Homo sapiens.
XX
PN   WO200264057-A2.
XX
PD   22-AUG-2002.
XX
PF   15-FEB-2002; 2002WO-US005212.
XX
PR   15-FEB-2001; 2001US-0268687P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Wang R;
XX
DR   WPI; 2002-627577/67.
XX
PT   Novel composition for treating a disease in an animal, comprises an
PT   immune effector cell and cell penetrating peptide associated with an
PT   antigen or antibody.
XX
PS   Disclosure; Page 17; 61pp; English.
XX
CC   The invention relates to a composition (I) comprising an immune effector
CC   cell and a cell penetrating peptide (CPP) associated with an antigen or
CC   antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC   with an antigen, and a pharmaceutically acceptable carrier and (2)
CC   preparing a composition for a disease, by providing (I) and CPP
CC   associated with an antigen for disease, and introducing the antigen-
CC   associated CPP to (I), where antigen enters into the cell. The antigens
CC   are, for example, tumour antigen derived epitopes recognised by tumour
CC   infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC   or II. The composition is useful for enhancing immunity in an animal to a
CC   disease, by administering a mature dendritic cell comprising CPP
CC   associated with an antigen to disease, to the animal, such that following
CC   the administration, animal is protected from disease, where the animal
CC   comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC   disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC   cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC   cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC   breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC   The animal is further subjected to a cancer treatment including surgery,
CC   radiation, chemotherapy or gene therapy. The administration of (I),
CC   preferably dendritic cell is prior to, subsequent to or concurrent with,
CC   the cancer treatment. The present sequence is a tumour antigen derived
CC   epitope for inclusion in the composition of the invention
XX
SQ   Sequence 9 AA;

  Query Match             92.2%;  Score 47;  DB 5;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGDF 9
              |:|||||||
Db          1 DFMIQGGDF 9
```

```
RESULT 8
ABR84374
ID   ABR84374 standard; peptide; 9 AA.
XX
AC   ABR84374;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human CypB HLA-A24 epitope, SEQ ID NO:24.
XX
KW   Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW   cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW   immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW   human; human leukocyte antigen; HLA-A24 epitope.
XX
OS   Homo sapiens.
XX
PN   JP2002365286-A.
XX
PD   18-DEC-2002.
XX
PF   18-SEP-2001; 2001JP-00283413.
XX
PR   13-NOV-2000; 2000JP-00345094.
XX
PA   (ITOY/) ITO Y.
XX
DR   WPI; 2003-508315/48.
XX
PT   A detection method of antigen specific T-cells, comprises the use of
PT   plural antigenic peptides, useful in semi-quantitative determination of
PT   cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS   Example 8; Page 10; 18pp; Japanese.
XX
CC   The invention relates to a method for the detection of antigen specific T
CC   -cells in a blood sample involving the use of a plurality of antigenic
CC   peptides. The method comprises sampling of peripheral blood monocytes;
CC   stimulation of the collected peripheral blood monocytes with antigens
CC   without direct use of antigen presenting cells; and detection of T-cells
CC   specific to the antigen in the stimulated monocytes. The method is
CC   particularly used for the detection of cancer as it can be used in semi-
CC   quantitative determination of cancer specific T-cells. It can also be
CC   used for cancer vaccine therapy for patients with cervical or prostate
CC   cancer. The method can additionally be used to monitor of cellular
CC   immunity and cancer immune therapy by detection of specific T-cell
CC   frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC   leukocyte antigen) peptides of human origin used in an example from the
CC   invention
XX
SQ   Sequence 9 AA;

  Query Match             92.2%;  Score 47;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGDF 9
              |:|||||||
Db          1 DFMIQGGDF 9
```

RESULT 9
ADC17702
ID ADC17702 standard; peptide; 9 AA.
XX
AC ADC17702;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cyclophilin B protein amino acids 91-99.
XX
KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX
PN WO2003020306-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002WO-JP008641.
XX
PR 29-AUG-2001; 2001JP-00260046.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Yamada A;
XX
DR WPI; 2003-300831/29.
XX
PT Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 2; 49pp; Japanese.
XX
CC The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet dos not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 91-99 of the cyclophilin B protein.
XX
SQ Sequence 9 AA;

Query Match 92.2%; Score 47; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 10
ADG89642
ID ADG89642 standard; peptide; 9 AA.
XX
AC ADG89642;
XX
DT 11-MAR-2004 (first entry)
XX
DE Class I HLA-restricted widely expressed antigen #7.
XX
KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS Unidentified.
XX
PN WO2003100027-A2.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-US016736.
XX
PR 28-MAY-2002; 2002US-0383530P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2004-035134/03.
XX
PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
PS Disclosure; SEQ ID NO 85; 137pp; English.
XX
CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted widely expressed
CC antigen.
XX
SQ Sequence 9 AA;

Query Match 92.2%; Score 47; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 11
AAY69958
ID AAY69958 standard; peptide; 9 AA.
XX
AC AAY69958;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #38.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.

```
XX
PS   Claim 4; Page 61; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             80.4%;  Score 41;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGD 8
              |:||||||
Db          1 DFMIQGGD 8


RESULT 12
AAY69961
ID   AAY69961 standard; peptide; 9 AA.
XX
AC   AAY69961;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #41.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /label= Phe, Tyr, Met, Trp
FT   Misc-difference 9
FT                   /label= Phe, Leu, Ile, Trp, Met
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 10; Page 60; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             72.5%;  Score 37;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYMIQGGD 8
              | ||||||
Db          1 DXMIQGGD 8


RESULT 13
AAY69957
ID   AAY69957 standard; peptide; 9 AA.
XX
AC   AAY69957;
XX
DT   11-APR-2000  (first entry)
XX
DE   Human cyclophilin B peptide fragment #37.
XX
KW   Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW   HLA antigen; diagnosis; tumour; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9967288-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003360.
XX
PR   25-JUN-1998;   98JP-00178449.
XX
PA   (SUMU ) SUMITOMO PHARM CO LTD.
PA   (ITOH/) ITOH K.
XX
PI   Itoh K,  Gomi S;
XX
DR   WPI; 2000-116932/10.
XX
PT   Tumor antigen peptides derived from cyclophilin B for treatment and
PT   diagnosis of tumors.
XX
PS   Claim 4; Page 61; 64pp; Japanese.
XX
CC   This sequence represents a cyclophilin B peptide of the invention. The
CC   peptides are tumour antigen peptides derived from cyclophilin B, that
CC   recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC   peptides are used for the treatment and diagnosis of tumours
XX
SQ   Sequence 9 AA;

  Query Match             70.6%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YMIQGGDF 9
              :| |||||
Db          2 FMCQGGDF 9


RESULT 14
AAR91898
ID   AAR91898 standard; protein; 12 AA.
XX
AC   AAR91898;
XX
DT   03-DEC-1996  (first entry)
XX
DE   KGF-b minor component N-terminal fragment.
XX
KW   Keratinocyte growth factor; KGF; Cys1; Cys15; deletion; substitution;
KW   Met-KGF analog; stimulate; non-fibroblast epithelial cell; antibody;
KW   detection; purification; adnexal structure; hair follicle; sweat gland;
KW   sebaceous gland; burn; gastric ulcer; duodenal ulcer; liver function;
KW   hepatic cirrhosis; ss.
XX
OS   Synthetic.
XX
PN   WO9611949-A2.
```

XX
PD 25-APR-1996.
XX
PF 12-OCT-1995; 95WO-IB000971.
XX
PR 13-OCT-1994; 94US-00323340.
PR 13-OCT-1994; 94US-00323475.
PR 07-JUN-1995; 95US-00487825.
XX
PA (AMGE-) AMGEN INC.
XX
PI Morris CF, Kenney WC, Chen B, Hsu EW;
XX
DR WPI; 1996-221944/22.
XX
PT Keratinocyte growth factor analogues with modified N-terminal region -
PT stimulate prodn. of non-fibroblast epithelial cells and are useful e.g.
PT to treat gastric and duodenal ulcers.
XX
PS Example 3; Page 52; 118pp; English.
XX
CC The sequences given in AAR91897-98 represent the N-terminal peptides from
CC the major and minor components, KGF-a and KGF-b, of recombinantly
CC expressed keratinocyte growth factor (KGF). Interestingly the N-terminal
CC fragment of KGF-b indicates that it is an N-terminally truncated form of
CC KGF which is proteolytically cleaved at the Arg23-Ser24 peptide bond. KGF
CC may be used in the construction of KGF analogues (see also AAR91865-96).
CC These analogues have up to the first 24 N-terminal amino acids modified
CC so that Cys1 and Cys15 are deleted or substituted. Deleting or
CC substituting the Cys residues at positions 1 and 15 of native KGF
CC produces a KGF analogue which has substantially improved stability. These
CC KGF analogues can be used to stimulate the production of non-fibroblast
CC epithelial cells. They are useful as therapeutic, diagnostic and research
CC agents and in the generation of antibodies for the detection or
CC purification of native KGF. The KGF analogues may be applied to tissues
CC with damage to, or insufficient numbers of, non-fibroblast epithelium
CC cells. This includes the stimulation, proliferation and differentiation
CC of adnexal structures, e.g. hair follicles, sweat glands, and sebaceous
CC glands in burns patients, treating gastric and duodenal ulcers, and
CC increasing liver function to treat or prevent e.g. hepatic cirrhosis
XX
SQ Sequence 12 AA;

Query Match 53.9%; Score 27.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 DYMIQGGD 8
              ||| :|||
Db          3 DYM-EGGD 9
```

RESULT 15
AAR45361
ID AAR45361 standard; peptide; 9 AA.
XX
AC AAR45361;
XX
DT 16-OCT-2003 (revised)
DT 04-JUL-1994 (first entry)
XX
DE Choline oxidase N-terminal.
XX
KW Preparation; high; purity; yield; chemical analysis; esterase;
KW determination; phospholipid.
XX
OS Saccharomonospora glauca.
XX
PN JP05317056-A.
XX
PD 03-DEC-1993.
XX
PF 22-JAN-1993; 93JP-00008835.
XX
PR 22-JAN-1992; 92JP-00009256.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
DR WPI; 1994-011021/02.
XX
PT DNA fragment for choline oxidase prepn., for high purity and high yield -
PT comprises gene coding choline oxidase prepd. by culturing microbe
PT transformed by recombinant plasmid for choline chemical analysis and
PT choline esterase determn.
XX
PS Claim 5; Page 2; 8pp; Japanese.
XX
CC The sequence is that of the N-terminal of choline oxidase. Choline
CC oxidase is useful for chemical analysis of choline, determination of
CC choline esterase contained in serum and determination of phospholipid.
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 9 AA;

Query Match 52.9%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DYMIQGG 7
              ||:: ||
Db          3 DYVVVGG 9
```

Search completed: October 21, 2004, 07:21:04
Job time : 84 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	25	49.0	9	1	US-08-457-172-1	Sequence 1, Appli
2	25	49.0	12	2	US-08-406-330-75	Sequence 75, Appl
3	25	49.0	12	2	US-08-556-597-75	Sequence 75, Appl
4	24	47.1	8	2	US-08-459-568-75	Sequence 75, Appl
5	24	47.1	8	2	US-08-399-411-75	Sequence 75, Appl
6	24	47.1	8	3	US-08-516-859A-75	Sequence 75, Appl
7	24	47.1	8	3	US-09-586-472-75	Sequence 75, Appl
8	24	47.1	8	4	US-09-528-706-75	Sequence 75, Appl
9	24	47.1	10	3	US-08-765-953-8	Sequence 8, Appli
10	24	47.1	10	6	5196404-18	Patent No. 5196404
11	24	47.1	10	6	5433940-25	Patent No. 5433940
12	24	47.1	12	4	US-09-846-350A-1	Sequence 1, Appli
13	23.5	46.1	11	1	US-07-620-426B-19	Sequence 19, Appl
14	23.5	46.1	11	1	US-07-662-007B-19	Sequence 19, Appl
15	23.5	46.1	11	1	US-07-824-247-19	Sequence 19, Appl
16	23.5	46.1	11	3	US-08-470-204A-19	Sequence 19, Appl
17	23	45.1	8	1	US-08-487-860-62	Sequence 62, Appl
18	23	45.1	10	1	US-08-658-130-21	Sequence 21, Appl
19	23	45.1	10	5	PCT-US96-08723-21	Sequence 21, Appl
20	23	45.1	12	3	US-09-188-579-51	Sequence 51, Appl
21	23	45.1	12	3	US-09-329-350-27	Sequence 27, Appl
22	23	45.1	12	3	US-09-315-444-51	Sequence 51, Appl
23	23	45.1	12	4	US-09-721-362-51	Sequence 51, Appl
24	23	45.1	12	4	US-09-752-165-71	Sequence 71, Appl
25	23	45.1	12	4	US-08-841-636A-27	Sequence 27, Appl
26	22	43.1	8	1	US-08-266-514-17	Sequence 17, Appl
27	22	43.1	8	2	US-08-654-604-17	Sequence 17, Appl
28	22	43.1	9	1	US-08-215-805A-7	Sequence 7, Appli
29	22	43.1	9	1	US-08-215-805A-52	Sequence 52, Appl
30	22	43.1	9	1	US-08-215-805A-58	Sequence 58, Appl
31	22	43.1	9	2	US-08-637-759B-444	Sequence 444, App
32	22	43.1	9	3	US-08-871-355A-444	Sequence 444, App
33	22	43.1	9	3	US-09-201-945-444	Sequence 444, App
34	22	43.1	11	3	US-09-026-276-23	Sequence 23, Appl
35	22	43.1	11	4	US-09-964-201A-23	Sequence 23, Appl
36	22	43.1	12	1	US-08-082-849B-15	Sequence 15, Appl
37	22	43.1	12	4	US-09-785-921A-13	Sequence 13, Appl
38	22	43.1	12	5	PCT-US94-01624-15	Sequence 15, Appl
39	21.5	42.2	9	1	US-08-410-941-17	Sequence 17, Appl
40	21.5	42.2	9	1	US-08-468-546-17	Sequence 17, Appl
41	21.5	42.2	9	2	US-08-468-547-17	Sequence 17, Appl
42	21.5	42.2	9	2	US-08-467-937-17	Sequence 17, Appl
43	21.5	42.2	9	3	US-09-074-950-17	Sequence 17, Appl
44	21.5	42.2	9	4	US-09-573-068-17	Sequence 17, Appl
45	21.5	42.2	12	1	US-08-410-941-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-457-172-1
; Sequence 1, Application US/08457172
; Patent No. 5622837
; GENERAL INFORMATION:
; APPLICANT: Hans Scheefers, Ursula Scheefers-Borchel and
; APPLICANT: Andreas Sziegoleit
; TITLE OF INVENTION: PANCREAS ELASTASE 1-SPECIFIC ANTIBODY, A PROCESS FOR
; TITLE OF INVENTION: OBTAINING IT, AND A TEST KIT CONTAINING SUCH ANTIBODY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,172
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,395
; FILING DATE:
; APPLICATION NUMBER: US 07/969,173
; FILING DATE: 29-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42883/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: pancreatic
US-08-457-172-1

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  Query Match             49.0%;  Score 25;  DB 1;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3.8e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |: |||
Db          2 MVAGGD 7


RESULT 2
US-08-406-330-75
; Sequence 75, Application US/08406330
; Patent No. 5817748
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Jonathan L.
;    APPLICANT:  Lyle, Vicki A.
;    TITLE OF INVENTION:  MIMOTOPES AND ANTI-MIMOTOPES OF
;    TITLE OF INVENTION:  HUMAN PLATELET GLYCOPROTEIN Ib/IX
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/406,330
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  20884/100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-406-330-75

  Query Match             49.0%;  Score 25;  DB 2;  Length 12;
  Best Local Similarity   37.5%;  Pred. No. 1.6e+02;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YMIQGGDF 9
              ::::|| |
Db          1 FVVRGGTF 8


RESULT 3
US-08-556-597-75
; Sequence 75, Application US/08556597
; Patent No. 5877155
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Jonathan L.
;    APPLICANT:  Lyle, Vicki A.
;    TITLE OF INVENTION:  MIMOTOPES AND ANTI-MIMOTOPES OF
;    TITLE OF INVENTION:  HUMAN PLATELET GLYCOPROTEIN Ib/IX
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/556,597
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/406,330
;      FILING DATE:  17-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Timian, Susan J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  20884/101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1636
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-556-597-75

  Query Match             49.0%;  Score 25;  DB 2;  Length 12;
  Best Local Similarity   37.5%;  Pred. No. 1.6e+02;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YMIQGGDF 9
              ::::|| |
Db          1 FVVRGGTF 8


RESULT 4
US-08-459-568-75
; Sequence 75, Application US/08459568
; Patent No. 5811304
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,568
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
```

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;       REFERENCE/DOCKET NUMBER:  P-LJ 1264
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619) 535-9001
;       TELEFAX:  (619) 535-8949
;   INFORMATION FOR SEQ ID NO:  75:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-459-568-75

  Query Match             47.1%;  Score 24;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              :::|||
Db          3 LLEGGD 8


RESULT 5
US-08-399-411-75
; Sequence 75, Application US/08399411
; Patent No. 5831008
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/399,411
;      FILING DATE:  06-MAR-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-399-411-75

  Query Match             47.1%;  Score 24;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              :::|||
Db          3 LLEGGD 8


RESULT 6
US-08-516-859A-75
; Sequence 75, Application US/08516859A
; Patent No. 6069231
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/516,859A
;      FILING DATE:  18-AUG-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/292,683
;      FILING DATE:  18-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-516-859A-75

  Query Match             47.1%;  Score 24;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              :::|||
Db          3 LLEGGD 8


RESULT 7
US-09-586-472-75
; Sequence 75, Application US/09586472
; Patent No. 6323335
;  GENERAL INFORMATION:
;       APPLICANT: Huang, Shi
;       TITLE OF INVENTION: Retinoblastoma Protein - Interacting
;                           Zinc Finger Proteins
;       NUMBER OF SEQUENCES: 106
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Campbell & Flores LLP
;            STREET: 4370 La Jolla Village Drive, Suite 700
;            CITY: San Diego
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92122
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/586,472
;            FILING DATE: 01-Jun-2000
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;           CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 09/528,706
;           FILING DATE: 17-MAR-2000
;           APPLICATION NUMBER: US 08/516,859
;           FILING DATE: 18-AUG-1995
;           APPLICATION NUMBER: US 08/399,411
;           FILING DATE: 06-MAR-1995
;           APPLICATION NUMBER: US 08/292,683
;           FILING DATE: 18-AUG-1994
;         ATTORNEY/AGENT INFORMATION:
;           NAME: Campbell, Cathryn A.
;           REGISTRATION NUMBER: 31,815
;           REFERENCE/DOCKET NUMBER: P-LJ 4130
;         TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (619) 535-9001
;           TELEFAX: (619) 535-8949
;    INFORMATION FOR SEQ ID NO: 75:
;         SEQUENCE CHARACTERISTICS:
;           LENGTH: 8 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-586-472-75

  Query Match             47.1%;  Score 24;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              :::|||
Db          3 LLEGGD 8


RESULT 8
US-09-528-706-75
; Sequence 75, Application US/09528706
; Patent No. 6468985
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/528,706
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/516,859
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/292,683
;      FILING DATE:  18-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-528-706-75

  Query Match             47.1%;  Score 24;  DB 4;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 3.8e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              :::|||
Db          3 LLEGGD 8


RESULT 9
US-08-765-953-8
; Sequence 8, Application US/08765953
; Patent No. 6342201
;  GENERAL INFORMATION:
;    APPLICANT:  DINKELBORG, LUDGER
;    APPLICANT:  STEPHAN, CHRISTOPH
;    APPLICANT:  SEMMLER, WOLFHARD
;    APPLICANT:  SPECK, ULRICH
;    APPLICANT:  KENKLEIN, PETER
;    TITLE OF INVENTION:  COMPLEX COMPOUNDS FOR DIAGNOSIS OF
;    TITLE OF INVENTION:  VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOOD, PHILLIPS, VAN SANTEN, CLARK & MORTIMER
;      STREET:  500 West Madison Street, Suite 3800
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60661-2511
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  COMPAQ ProLinea 4/25s
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect for Windows 6.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,953
;      FILING DATE:  17-JULY-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/DE95/00837
;      FILING DATE:  21-JUNE-1995
;      APPLICATION NUMBER:  P 44 25 778.3
;      FILING DATE:  13-JULY-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mortimer, John S.
;      REGISTRATION NUMBER:  30,407
;      REFERENCE/DOCKET NUMBER:  1214.00001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/876-1800
;      TELEFAX:  312/876-2020
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-765-953-8

  Query Match             47.1%;  Score 24;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          6 GGDF 9
              ||||
Db          1 GGDF 4


RESULT 10
5196404-18
;Patent No. 5196404
;     APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
;     TITLE OF INVENTION: INHIBITORS OF THROMBIN
;     NUMBER OF SEQUENCES: 18
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/549,388
;       FILING DATE: 06-JUL-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 395,482
;       FILING DATE: 18-AUG-1989
;SEQ ID NO:18:
;       LENGTH: 10
5196404-18

  Query Match             47.1%;  Score 24;  DB 6;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 2e+02;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYMIQGG 7
              |:: :||
Db          2 DFLAEGG 8


RESULT 11
5433940-25
;Patent No. 5433940
;     APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
;     TITLE OF INVENTION: INHIBITORS OF THROMBIN
;     NUMBER OF SEQUENCES: 25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/834,259
;       FILING DATE: 17-AUG-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 548,388
;       FILING DATE: 06-JUL-1989
;       APPLICATION NUMBER: 395,482
;       FILING DATE: 18-AUG-1989
;SEQ ID NO:25:
;       LENGTH: 10
5433940-25

  Query Match             47.1%;  Score 24;  DB 6;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 2e+02;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYMIQGG 7
              |:: :||
Db          2 DFLAEGG 8


RESULT 12
US-09-846-350A-1
; Sequence 1, Application US/09846350A
; Patent No. 6599877
; GENERAL INFORMATION:
;  APPLICANT: Jackowski, George
;  APPLICANT:  Marshall, John
;  APPLICANT:  Vrees, Tammy
;  APPLICANT:  Thatcher, Brad
;  TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
;  TITLE OF INVENTION:  of 1020 Daltons
;  FILE REFERENCE: 2132.025
;  CURRENT APPLICATION NUMBER: US/09/846,350A
;  CURRENT FILING DATE:  2001-04-30
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-846-350A-1

  Query Match             47.1%;  Score 24;  DB 4;  Length 12;
  Best Local Similarity   42.9%;  Pred. No. 2.5e+02;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYMIQGG 7
              |:: :||
Db          2 DFLAEGG 8


RESULT 13
US-07-620-426B-19
; Sequence 19, Application US/07620426B
; Patent No. 5298421
;  GENERAL INFORMATION:
;    APPLICANT:  Davies, Huw Maelor
;    APPLICANT:  Pollard, Michael Roman
;    APPLICANT:  Voekler, Toni Alois
;    TITLE OF INVENTION:  Plant Thioesterases
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Calgene, Inc.
;      STREET:  1920 Fifth Street
;      CITY:  Davis
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  95616
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 KB storage
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 6.0.7
;      SOFTWARE:  MicrosoftWord 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/620,426B
;      FILING DATE:  19901130
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/514,030
;      FILING DATE:  26-APRIL-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth Lassen
;      REGISTRATION NUMBER:  31,845
;      NAME:  Donna E. Scherer
;      REGISTRATION NUMBER:  34,719
;      REFERENCE/DOCKET NUMBER:  CGNE 70-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  916-753-6313
;      TELEFAX:  916-753-1510
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-620-426B-19

  Query Match             46.1%;  Score 23.5;  DB 1;  Length 11;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 DYMIQGG 7
              || ||||
Db          1 DY-IQGG 6


RESULT 14
US-07-662-007B-19
; Sequence 19, Application US/07662007B
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; Patent No. 5344771
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Maelor
; APPLICANT: Pollard, Michael Roman
; APPLICANT: Voekler, Toni Alois
; APPLICANT: Thompson, Gregory A.
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,007B
; FILING DATE: 19910408
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: CGNE 70-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-662-007B-19

Query Match 46.1%; Score 23.5; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DYMIQGG 7
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Db 1 DY-IQGG 6

RESULT 15
US-07-824-247-19
; Sequence 19, Application US/07824247
; Patent No. 5512482
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/824,247
; FILING DATE: 19920122
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/704,861
; FILING DATE: 21-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02960
; FILING DATE: 25-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,007
; FILING DATE: 27-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 82-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-824-247-19

Query Match 46.1%; Score 23.5; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DYMIQGG 7
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Db 1 DY-IQGG 6

Search completed: October 21, 2004, 07:29:31
Job time : 22.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	9	16	US-10-788-016-9	Sequence 9, Appli
2	47	92.2	9	15	US-10-447-161-85	Sequence 85, Appl
3	47	92.2	9	16	US-10-788-016-2	Sequence 2, Appli
4	26	51.0	10	10	US-09-573-822C-257	Sequence 257, App
5	26	51.0	12	14	US-10-320-231A-18	Sequence 18, Appl
6	25	49.0	9	15	US-10-057-475B-10856	Sequence 10856, A
7	25	49.0	9	15	US-10-057-475B-10911	Sequence 10911, A
8	25	49.0	9	15	US-10-154-884B-10856	Sequence 10856, A
9	25	49.0	9	15	US-10-154-884B-10911	Sequence 10911, A
10	25	49.0	9	15	US-10-363-791-103	Sequence 103, App
11	25	49.0	9	15	US-10-182-252A-872	Sequence 872, App
12	24	47.1	10	9	US-09-846-350-1	Sequence 1, Appli
13	24	47.1	11	9	US-09-846-342-1	Sequence 1, Appli
14	24	47.1	11	15	US-10-356-257-161	Sequence 161, App
15	24	47.1	12	9	US-09-845-725-1	Sequence 1, Appli
16	23	45.1	9	15	US-10-182-252A-281	Sequence 281, App
17	23	45.1	9	15	US-10-182-252A-282	Sequence 282, App
18	23	45.1	9	15	US-10-182-252A-878	Sequence 878, App
19	23	45.1	9	15	US-10-182-252A-879	Sequence 879, App
20	23	45.1	9	15	US-10-182-252A-880	Sequence 880, App
21	23	45.1	9	15	US-10-182-252A-881	Sequence 881, App
22	23	45.1	9	15	US-10-182-252A-882	Sequence 882, App
23	23	45.1	9	15	US-10-182-252A-883	Sequence 883, App
24	23	45.1	11	9	US-09-791-378-497	Sequence 497, App
25	23	45.1	11	9	US-09-791-378-546	Sequence 546, App
26	23	45.1	11	9	US-09-791-378-583	Sequence 583, App
27	23	45.1	11	9	US-09-826-290-337	Sequence 337, App
28	23	45.1	11	10	US-09-791-393-216	Sequence 216, App
29	23	45.1	11	10	US-09-791-389-216	Sequence 216, App
30	23	45.1	11	11	US-09-791-377-497	Sequence 497, App
31	23	45.1	11	11	US-09-791-377-546	Sequence 546, App
32	23	45.1	11	11	US-09-791-377-583	Sequence 583, App
33	23	45.1	11	14	US-10-076-047A-55	Sequence 55, Appl
34	23	45.1	11	15	US-10-264-309-466	Sequence 466, App
35	23	45.1	12	8	US-08-841-636A-27	Sequence 27, Appl
36	23	45.1	12	14	US-10-167-831-71	Sequence 71, Appl
37	23	45.1	12	16	US-10-782-002-27	Sequence 27, Appl
38	23	45.1	12	16	US-10-825-378-27	Sequence 27, Appl
39	22	43.1	9	15	US-10-182-252A-891	Sequence 891, App
40	22	43.1	9	15	US-10-182-252A-892	Sequence 892, App
41	22	43.1	9	15	US-10-182-252A-893	Sequence 893, App
42	22	43.1	9	15	US-10-182-252A-894	Sequence 894, App
43	22	43.1	9	15	US-10-182-252A-895	Sequence 895, App
44	22	43.1	9	15	US-10-182-252A-896	Sequence 896, App
45	22	43.1	9	15	US-10-182-252A-897	Sequence 897, App

ALIGNMENTS

RESULT 1
US-10-788-016-9
; Sequence 9, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
; OTHER INFORMATION: residues from the 91st residue to the 99th residue of
; OTHER INFORMATION: cyclophillin B
US-10-788-016-9

Query Match 100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|||||||||
Db 1 DYMIQGGDF 9

RESULT 2
US-10-447-161-85

; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match 92.2%; Score 47; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 3
US-10-788-016-2
; Sequence 2, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
; OTHER INFORMATION: to the 99th residue of cyclophillin B
US-10-788-016-2

Query Match 92.2%; Score 47; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQGGDF 9
|:|||||||
Db 1 DFMIQGGDF 9

RESULT 4
US-09-573-822C-257
; Sequence 257, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 257
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG024 at 351-360 and may interact with Sequenc
; OTHER INFORMATION: in this patent.
US-09-573-822C-257

Query Match 51.0%; Score 26; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIQGGD 8
:|:|: ||
Db 1 NYLIKDGD 8

RESULT 5
US-10-320-231A-18
; Sequence 18, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-18

Query Match 51.0%; Score 26; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YMIQGGDF 9
| : |||
Db 3 YFLYNGDF 10

RESULT 6
US-10-057-475B-10856
; Sequence 10856, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10856
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 long MHC HLA A2 class I binding peptide
US-10-057-475B-10856

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          4 IQGGDF 9
              :||| |
Db          2 LQGGSF 7
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RESULT 7
US-10-057-475B-10911
; Sequence 10911, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10911
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-057-475B-10911

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 IQGGDF 9
              :||| |
Db          2 LQGGSF 7
```

RESULT 8
US-10-154-884B-10856
; Sequence 10856, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10856
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 long MHC HLA A2 class I binding peptide
US-10-154-884B-10856

Query Match 49.0%; Score 25; DB 15; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 IQGGDF 9
              :||| |
Db          2 LQGGSF 7
```

RESULT 9
US-10-154-884B-10911
; Sequence 10911, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10911
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-154-884B-10911

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 IQGGDF 9
              :||| |
Db          2 LQGGSF 7
```

RESULT 10
US-10-363-791-103
; Sequence 103, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, Masato
; APPLICANT: KUZUMAKI, No. US20040029197A1oru
; APPLICANT: SATO, No. US20040029197A1iyuki
; APPLICANT: SAHARA, Hiroeki
; TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000-274218
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-103

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 DYMIQGGDF 9
              |  | | | ||
Db          1 DITIYGNDF 9
```

RESULT 11
US-10-182-252A-872
; Sequence 872, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 872
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-872

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 MIQGGDF 9
              ||| |:|
Db          1 MIQRGNF 7
```

RESULT 12
US-09-846-350-1
; Sequence 1, Application US/09846350
; Patent No. US20020161188A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular W
; TITLE OF INVENTION: of 1020 Daltons
; FILE REFERENCE: 2132.025
; CURRENT APPLICATION NUMBER: US/09/846,350

; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-350-1

Query Match 47.1%; Score 24; DB 9; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DYMIQGG 7
              |:: :||
Db          1 DFLAEGG 7
```

RESULT 13
US-09-846-342-1
; Sequence 1, Application US/09846342
; Patent No. US20020160422A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1077 DALTONS
; FILE REFERENCE: 2132.026
; CURRENT APPLICATION NUMBER: US/09/846,342
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-342-1

Query Match 47.1%; Score 24; DB 9; Length 11;
Best Local Similarity 42.9%; Pred. No. 9.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DYMIQGG 7
              |:: :||
Db          2 DFLAEGG 8
```

RESULT 14
US-10-356-257-161
; Sequence 161, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-161

Query Match 47.1%; Score 24; DB 15; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 YMIQGG 7
              :|::||
Db          6 FMVRGG 11
```

RESULT 15
US-09-845-725-1
; Sequence 1, Application US/09845725
; Patent No. US20020161185A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR W
; TITLE OF INVENTION: OF 1206 DALTONS
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match 47.1%; Score 24; DB 9; Length 12;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 DYMIQGG 7
              |:: :||
Db          3 DFLAEGG 9
```

Search completed: October 21, 2004, 07:33:43
Job time : 61.75 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	45.1	11	2	B60769	Ig H2 chain - Paci
2	20	39.2	10	2	E60589	sperm-activating p
3	20	39.2	12	2	A61309	glycoprotein hormo
4	20	39.2	12	2	PH1458	T-cell receptor be
5	20	39.2	12	2	S43170	kinesin light chai
6	19	37.3	10	2	PN0165	triose-phosphate i
7	19	37.3	10	2	F33932	Ig mu chain J regi
8	19	37.3	11	2	PU0029	33K protein 3218 -
9	19	37.3	12	2	S65730	hemoglobin, extrac
10	18	35.3	7	2	PT0542	T-cell receptor be
11	18	35.3	8	2	PQ0012	cholecystokinin -
12	18	35.3	8	2	A43001	cholecystokinin -
13	18	35.3	8	2	JS0318	leucokinin VIII -
14	18	35.3	9	2	QDRB	delta sleep-induci
15	18	35.3	11	2	PT0250	Ig heavy chain CRD
16	18	35.3	11	2	PH1343	Ig heavy chain DJ
17	18	35.3	11	2	S60354	retinal oxidase -
18	18	35.3	11	2	PN0044	protein kinase C i
19	18	35.3	11	2	PT0218	T-cell receptor be
20	18	35.3	11	2	I41946	T-cell receptor ga
21	18	35.3	11	2	A61575	Trimeresurus serin
22	18	35.3	12	2	S26544	T-cell receptor be
23	17	33.3	3	3	A23751	spinal cord peptid
24	17	33.3	9	1	YFPG	thymic factor - pi
25	17	33.3	9	2	A60957	thymocyte growth p
26	17	33.3	10	2	E41946	T-cell receptor ga
27	17	33.3	10	2	A60589	sperm-activating p
28	17	33.3	11	2	S57575	T cell receptor V-
29	17	33.3	11	2	D37196	bradykinin-potenti
30	17	33.3	11	4	S19015	hypothetical prote
31	16	31.4	9	2	E41978	calliFMRFamide 5 -
32	16	31.4	9	2	F41978	calliFMRFamide 6 -
33	16	31.4	9	2	G41978	calliFMRFamide 7 -
34	16	31.4	10	2	C61440	polygalacturonase
35	16	31.4	10	2	S62880	polygalacturonase
36	16	31.4	10	2	A44871	monodehydroascorba
37	16	31.4	10	2	C60787	sperm-activating p
38	16	31.4	10	2	A60588	sperm-activating p
39	16	31.4	10	2	C60527	sperm-activating p
40	16	31.4	10	2	E39572	sperm-activating p
41	16	31.4	10	2	D60589	sperm-activating p
42	16	31.4	12	2	S26541	T-cell receptor be
43	16	31.4	12	2	PH1606	Ig H chain V-D-J r
44	16	31.4	12	2	S23168	Z protein - guinea
45	16	31.4	12	2	T46794	hypothetical prote

ALIGNMENTS

RESULT 1
B60769
Ig H2 chain - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C;Accession: B60769
R;Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A;Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A;Reference number: A60769; MUID:91060965; PMID:2123225
A;Accession: B60769
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HAN>

Query Match 45.1%; Score 23; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DYMIQ 5
              |:|||
Db          5 DFMIQ 9
```

RESULT 2
E60589
sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I) - Echinometra mathaei
C;Species: Echinometra mathaei
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C;Accession: E60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguch
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pep
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: E60589
A;Molecule type: protein
A;Residues: 1-10 <YOS>
A;Cross-references: UNIPROT:Q7M4C1
A;Note: an identical peptide was isolated from Echinometra mathaei type A and type B

Query Match 39.2%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 YMIQGG 7
              | : ||
Db          2 YSLSGG 7
```

RESULT 3
A61309

glycoprotein hormones alpha chain - hamster (fragment)
N;Alternate names: choriogonadotropin alpha chain; luteinizing hormone alpha chain; lutr
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61309
R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.
Endocrinology 111, 1263-1269, 1982
A;Title: Isolation and characterization of hamster luteinizing hormone.
A;Reference number: A61309; MUID:83003498; PMID:6889489
A;Accession: A61309
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <GLE>
A;Cross-references: UNIPROT:Q7M0A7
C;Superfamily: glycoprotein hormones alpha chain
C;Keywords: glycoprotein

Query Match 39.2%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIQG 6
|: :||
Db 5 DFTMQG 10

RESULT 4
PH1458
T-cell receptor beta chain (clone 332/1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C;Accession: PH1458; S26543
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1458
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Experimental source: cytolytic T-lymphocyte, clone 332/1K
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: S26543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CA2>
A;Cross-references: EMBL:X67993
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/C44
C;Keywords: receptor; T-cell

Query Match 39.2%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QGGDF 9
|| |:
Db 5 QGSDY 9

RESULT 5
S43170
kinesin light chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: S43170
R;Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
submitted to the EMBL Data Library, December 1992
A;Description: Promoter first exon/intron characterization and chromosomal location of t
A;Reference number: S43170
A;Accession: S43170
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-12 <CHE>
A;Cross-references: UNIPROT:Q13865; EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g4687

Query Match 39.2%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MIQGG 7
|::||
Db 1 MLRGG 5

RESULT 6
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: PN0165
R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PN0160
A;Accession: PN0165
A;Molecule type: protein
A;Residues: 1-10 <FUK>
A;Cross-references: UNIPROT:Q7M4X7
A;Experimental source: strain M-1-1
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGDF 9
||:|
Db 7 GGNF 10

RESULT 7
F33932
Ig mu chain J region (E7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: F33932
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-li
A;Reference number: A33932; MUID:89282823; PMID:2499887
A;Accession: F33932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <BAC>
A;Cross-references: UNIPROT:Q99NG4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q1; UNIPR
PROT:Q9DCD9; UNIPROT:Q924R0; UNIPROT:Q8K172; UNIPROT:Q99LA6; UNIPROT:Q91X92; GB:M27106
C;Keywords: immunoglobulin

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYMIQG 6
|| ||
Db 3 DYWGQG 8

RESULT 8
PU0029
33K protein 3218 - rice (strain Nohonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PU0029
R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PU0029
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: bran
C;Comment: molecular weight 33K, pI 6.0.

Query Match 37.3%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QGGDF 9
:|| |
Db 3 EGGPF 7

RESULT 9
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65730
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65730
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FUS>

Query Match 37.3%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYMIQ 5
|::||
Db 7 DHLIQ 11

RESULT 10
PT0542
T-cell receptor beta chain V-D-J region (126-1BA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0542
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0542
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
|||
Db 3 GGD 5

RESULT 11
PQ0012
cholecystokinin - southeastern quoll
N;Alternate names: CCK
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: PQ0012
A;Molecule type: protein
A;Residues: 1-8 <FAN>
A;Cross-references: UNIPROT:P30369
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYM 3
|||
Db 1 DYM 3

RESULT 12
A43001
cholecystokinin - tammar wallaby
N;Alternate names: CCK
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004
C;Accession: A43001; PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: A43001
A;Molecule type: protein
A;Residues: 1-8 <FAN>
A;Cross-references: UNIPROT:P30369
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYM 3
|||
Db 1 DYM 3

RESULT 13
JS0318
leucokinin VIII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0318
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fina
A;Reference number: JS0317
A;Accession: JS0318
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19990
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile acti
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.3%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 GGDF 9
              | ||
Db          1 GADF 4


RESULT 14
QDRB
delta sleep-inducing peptide - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C;Accession: A01422
R;Monnier, M.; Dudler, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.
Experientia 33, 548-552, 1977
A;Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original
A;Reference number: A01422; MUID:77185324; PMID:862769
A;Accession: A01422
A;Molecule type: protein
A;Residues: 1-9 <MON>
A;Cross-references: UNIPROT:P01158
C;Comment: This peptide was obtained from dialysates of occipital venous sinus blood frc
 of recipient rabbits, it induces spindle and delta EEG activity and reduced motor activ

  Query Match             35.3%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGD 8
              |||
Db          3 GGD 5


RESULT 15
PT0250
Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0250
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0250
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

  Query Match             35.3%;  Score 18;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GDF 9
              |||
Db          4 GDF 6


Search completed: October 21, 2004, 07:28:00
Job time : 16.75 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	45.1	7	2	Q63480	Q63480 rattus norv
2	22	43.1	9	2	Q9PS68	Q9ps68 gallus gall
3	22	43.1	12	2	Q9H3W2	Q9h3w2 homo sapien
4	21	41.2	11	2	Q70Y64	Q70y64 plectranthu
5	21	41.2	11	2	CAD45529	Cad45529 plectrant
6	21	41.2	12	2	Q70Y58	Q70y58 clinopodium
7	21	41.2	12	2	CAD45546	Cad45546 clinopodi
8	20	39.2	8	2	Q70Y88	Q70y88 platostoma
9	20	39.2	8	2	CAD45489	Cad45489 platostom
10	20	39.2	10	2	Q7M4C1	Q7m4c1 echinometra
11	20	39.2	12	2	Q13865	Q13865 homo sapien
12	20	39.2	12	2	Q7M0A7	Q7m0a7 cricetidae
13	19	37.3	7	2	O55184	O55184 rattus norv
14	19	37.3	10	2	Q7M4X7	Q7m4x7 fusarium sp
15	19	37.3	10	2	Q8UVW2	Q8uvw2 oreochromis
16	19	37.3	11	2	Q9HFN8	Q9hfn8 candida rug
17	19	37.3	11	2	O77876	O77876 oreochromis
18	19	37.3	11	2	Q70Y98	Q70y98 capitanopsi
19	19	37.3	11	2	CAD45456	Cad45456 capitanop
20	19	37.3	12	2	Q8UVV8	Q8uvv8 squalus aca
21	19	37.3	12	2	Q8UVW0	Q8uvw0 rana catesb
22	18	35.3	8	1	CCKN_MACEU	P30369 macropus eu
23	18	35.3	8	1	LCK8_LEUMA	P19990 leucophaea
24	18	35.3	8	1	LMT2_LOCMI	P22396 locusta mig
25	18	35.3	8	2	Q9TT78	Q9tt78 canis famil
26	18	35.3	9	1	DSIP_RABIT	P01158 oryctolagus
27	18	35.3	9	2	Q6LDH6	Q6ldh6 rattus norv
28	18	35.3	9	2	AAA40600	Aaa40600 rattus no
29	18	35.3	10	2	Q51812	Q51812 plasmid f.
30	18	35.3	11	2	O87882	O87882 mycobacteri
31	18	35.3	11	2	P83168	P83168 struthio ca
32	18	35.3	12	2	Q9N2B8	Q9n2b8 pongo pygma
33	18	35.3	12	2	Q9N2B9	Q9n2b9 gorilla gor
34	18	35.3	12	2	Q9N2C0	Q9n2c0 pan troglod
35	18	35.3	12	2	Q46712	Q46712 plasmid r10
36	17.5	34.3	10	1	ESTA_SCHGA	P81012 schizaphis
37	17	33.3	7	1	ASCL_ALLAS	P84071 allium asca
38	17	33.3	8	2	Q90ZV5	Q90zv5 fulica leuc
39	17	33.3	9	1	THYF_PIG	P01255 sus scrofa
40	17	33.3	9	2	Q7M3C5	Q7m3c5 ovis aries
41	17	33.3	10	1	AMPN_HELAM	P81731 helicoverpa
42	17	33.3	10	2	Q6LCI4	Q61ci4 homo sapien
43	17	33.3	10	2	Q96QA7	Q96qa7 homo sapien
44	17	33.3	10	2	Q7M4B7	Q7m4b7 heterocentr
45	17	33.3	10	2	Q8MJ52	Q8mj52 equus cabal

ALIGNMENTS

RESULT 1
Q63480
ID Q63480 PRELIMINARY; PRT; 7 AA.
AC Q63480;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
DR EMBL; U59125; AAB02827.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 45.1%; Score 23; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 IQGGD 8
              |:|||
Db          2 IRGGD 6
```

RESULT 2
Q9PS68
ID Q9PS68 PRELIMINARY; PRT; 9 AA.
AC Q9PS68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,

```
RA   Schneider W.J.;
RT   "The laying hen expresses two different low density lipoprotein
RT   receptor-related proteins.";
RL   J. Biol. Chem. 266:19079-19087(1991).
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1039 MW;  895EC68B5AB2CDC1 CRC64;

  Query Match             43.1%;  Score 22;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DYMIQ 5
              |||::
Db          5 DYMVK 9


RESULT 3
Q9H3W2
ID   Q9H3W2      PRELIMINARY;      PRT;    12 AA.
AC   Q9H3W2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   TRE17 protein.
GN   Name=TRE17 gene;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94010310; PubMed=8406013;
RA   Onno M., Nakamura T., Hillova J., Hill M.;
RT   "Identification of novel sequences in the repertoire of hypervariable
RT   TRE17 genes from immortalized nonmalignant and malignant human
RT   keratinocytes.";
RL   Gene 131:209-215(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93228825; PubMed=8471161;
RA   Onno M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.;
RT   "Human TRE17 oncogene is generated from a family of homologous
RT   polymorphic sequences by single-base changes.";
RL   DNA Cell Biol. 12:107-118(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hillova F.;
RL   Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X71371; CAC16150.1; -.
SQ   SEQUENCE   12 AA;  1252 MW;  6E17AFDE83ADD87B CRC64;

  Query Match             43.1%;  Score 22;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 2.7e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 MIQGGD 8
              |::|  |
Db          3 MVEGAD 8


RESULT 4
Q70Y64
ID   Q70Y64      PRELIMINARY;      PRT;    11 AA.
AC   Q70Y64;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   Name=rps16;
OS   Plectranthus ciliatus.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
OX   NCBI_TaxID=204208;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019625;
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505409; CAD45529.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1317 MW;  D8D98CB3AB587866 CRC64;

  Query Match             41.2%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 3.9e+03;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGG 7
              |  |||
Db          1 YGFQGG 6


RESULT 5
CAD45529
ID   CAD45529    PRELIMINARY;      PRT;    11 AA.
AC   CAD45529;
DT   14-MAR-2004 (TrEMBLrel. 27, Created)
DT   14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   RPS16.
OS   Plectranthus ciliatus.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
OX   NCBI_TaxID=204208;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505409; CAD45529.1; -.
KW   Chloroplast; Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1317 MW;  D8D98CB3AB587866 CRC64;

  Query Match             41.2%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 3.9e+03;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGG 7
              |  |||
Db          1 YGFQGG 6


RESULT 6
Q70Y58
ID   Q70Y58      PRELIMINARY;      PRT;    12 AA.
AC   Q70Y58;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   Name=rps16;
```

```
OS   Clinopodium vulgare subsp. arundanum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium.
OX   NCBI_TaxID=204223;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019625;
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505426; CAD45546.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1353 MW;  D43D1B51AF587866 CRC64;

  Query Match             41.2%;  Score 21;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGG 7
              ||||
Db          4 IQGG 7


RESULT 7
CAD45546
ID   CAD45546    PRELIMINARY;      PRT;    12 AA.
AC   CAD45546;
DT   14-MAR-2004 (TrEMBLrel. 27, Created)
DT   14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   RPS16.
OS   Clinopodium vulgare subsp. arundanum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium;
OC   Clinopodium vulgare.
OX   NCBI_TaxID=204223;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505426; CAD45546.1; -.
KW   Chloroplast; Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1353 MW;  D43D1B51AF587866 CRC64;

  Query Match             41.2%;  Score 21;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IQGG 7
              ||||
Db          4 IQGG 7


RESULT 8
Q70Y88
ID   Q70Y88      PRELIMINARY;      PRT;     8 AA.
AC   Q70Y88;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   Name=rps16;
OS   Platostoma fimbriatum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.
OX   NCBI_TaxID=204168;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15019625;
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505368; CAD45489.1; -.
DR   GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW   Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  789 MW;  86786772D1BB4772 CRC64;

  Query Match             39.2%;  Score 20;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGG 7
              | : ||
Db          3 YTVPGG 8


RESULT 9
CAD45489
ID   CAD45489    PRELIMINARY;      PRT;     8 AA.
AC   CAD45489;
DT   14-MAR-2004 (TrEMBLrel. 27, Created)
DT   14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Ribosomal protein (Fragment).
GN   RPS16.
OS   Platostoma fimbriatum.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.
OX   NCBI_TaxID=204168;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA   Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT   "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT   based on three plastid DNA regions.";
RL   Mol. Phylogenet. Evol. 31:277-299(2004).
DR   EMBL; AJ505368; CAD45489.1; -.
KW   Chloroplast; Ribosomal protein.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  789 MW;  86786772D1BB4772 CRC64;

  Query Match             39.2%;  Score 20;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+06;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGG 7
              | : ||
Db          3 YTVPGG 8


RESULT 10
Q7M4C1
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ID   Q7M4C1      PRELIMINARY;      PRT;    10 AA.
AC   Q7M4C1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I).
OS   Echinometra mathaei (Rock boring urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
OC   Echinometra.
OX   NCBI_TaxID=31178;
RN   [1]
RP   SEQUENCE.
RA   Yoshino K.I., Kajiura H., Nomura K., Takao T., Shimonishi Y.,
RA   Kurita M., Yamaguchi M., Suzuki N.;
RT   "A halogenated amino acid-containing sperm activating peptide and its
RT   related peptides isolated from the egg jelly of sea urchins,
RT   Tripneustes gratilla, Pseudoboletia maculata, Strongylocentrotus
RT   nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
RL   Comp. Biochem. Physiol. 94:739-751(1989).
DR   PIR; E60589; E60589.
SQ   SEQUENCE   10 AA;  925 MW;  8B9856D87865B735 CRC64;

  Query Match             39.2%;  Score 20;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+03;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGG 7
              | : ||
Db          2 YSLSGG 7


RESULT 11
Q13865
ID   Q13865      PRELIMINARY;      PRT;    12 AA.
AC   Q13865;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Kinesin light chain.
GN   Name=beta-kinesin;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97101110; PubMed=8945637;
RA   Chernajovsky Y., Brown A., Jones T.A.;
RT   "Promoter first exon/intron characterization and chromosomal location
RT   of the human light chain (beta) kinesin gene.";
RL   DNA Cell Biol. 15:965-974(1996).
DR   EMBL; X69658; CAA49349.1; -.
DR   PIR; S43170; S43170.
SQ   SEQUENCE   12 AA;  1274 MW;  3FB8D34EE165A5B8 CRC64;

  Query Match             39.2%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 6.7e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 MIQGG 7
              |::||
Db          1 MLRGG 5


RESULT 12
Q7M0A7
ID   Q7M0A7      PRELIMINARY;      PRT;    12 AA.
AC   Q7M0A7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Glycoprotein hormones alpha chain (Fragment).
OS   Cricetidae sp. (Hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
OX   NCBI_TaxID=36483;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83003498; PubMed=6889489;
RA   Glenn S.D., Nahm H.S., Greenwald G.S., Ward D.N.;
RT   "Isolation and characterization of hamster luteinizing hormone.";
RL   Endocrinology 111:1263-1269(1982).
DR   PIR; A61309; A61309.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1280 MW;  94A63728AA81A9CA CRC64;

  Query Match             39.2%;  Score 20;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 6.7e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DYMIQG 6
              |: :||
Db          5 DFTMQG 10


RESULT 13
O55184
ID   O55184      PRELIMINARY;      PRT;     7 AA.
AC   O55184;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orphan receptor TR4-NS (Fragment).
GN   Name=TR4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96198747; PubMed=8612486;
RA   Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA   Detera-Wadleigh S.D.;
RT   "Splice variants of rat TR4 orphan receptor: differential expression
RT   of novel sequences in the 5'-untranslated region and C-terminal
RT   domain.";
RL   Endocrinology 137:1562-1571(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96299786; PubMed=8661150;
RA   Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT   "New variants of the human and rat nuclear hormone receptor, TR4:
RT   expression and chromosomal localization of the human gene.";
RL   Genomics 35:361-366(1996).
DR   EMBL; U59454; AAB91433.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  663 MW;  6DDAA8787EB05350 CRC64;

  Query Match             37.3%;  Score 19;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 IQGGD 8
              | |||
Db          2 ICGGD 6


RESULT 14
Q7M4X7
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ID   Q7M4X7      PRELIMINARY;      PRT;    10 AA.
AC   Q7M4X7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Triose-phosphate isomerase (EC 5.3.1.1) (Fragment).
OS   Fusarium sporotrichioides.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX   NCBI_TaxID=5514;
RN   [1]
RP   SEQUENCE.
RA   Fukaya N., Chow L.P., Sugiura Y., Tsugita A., Ueno Y., Tabuchi K.;
RL   Submitted (MAY-1994) to the PIR data bank.
DR   PIR; PN0165; PN0165.
DR   GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1142 MW;  590E4D7862C9C9C3 CRC64;

  Query Match             37.3%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 8.8e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GGDF 9
              ||:|
Db          7 GGNF 10


RESULT 15
Q8UVW2
ID   Q8UVW2      PRELIMINARY;      PRT;    10 AA.
AC   Q8UVW2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   AMPA receptor subunit 2 alpha (Fragment).
GN   Name=GluR2a;
OS   Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; Oreochromis.
OX   NCBI_TaxID=8127;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21617183; PubMed=11741603;
RA   Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;
RT   "Q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript
RT   evolves no later than the appearance of cartilaginous fishes.";
RL   FEBS Lett. 509:277-281(2001).
DR   EMBL; AF350050; AAL57192.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1153 MW;  721A6E5AAEB866C4 CRC64;

  Query Match             37.3%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 8.8e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YMIQGGD 8
              :| || |
Db          1 FMRQGCD 7


Search completed: October 21, 2004, 07:26:51
Job time : 87 secs
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